79

152	26 212	46	66 332	86 392	106 452	126 512	146 572
A GCG	C H	C TGT	L	Y TAC	N AAT	G G	Q CAG
PCCT	H CAT	C TGC	F TTC	M ATG	P CCA	P CCG	PCCC
Q CAG	K AAG	D GAC	M	R CGC	P	G GGA	S TCA
R CGC	K AAA	E GAG	F	R AGG	Q CAG	G GGA	N AAC
R AGG	A GCC	Y TAC	Y TAC	R CGG	R AGG	P CCA	P
M ATG	E GAA	S TCC	\overline{W}	I ATC	T ACC	D GAC	P CCA
4GCC	T ACA	R CGC	L CIG	F	Y TAC	T ACT	V GTC
3AGGZ	C TGC	C TGC	R AGG	F	S	Y TAC	Q CAG
ACGC	EGAG	I ATA	Q CAG	G GGC	V GTG	Y TAT	F
GCTGGAGAGGACGCGAGGAGCC	$_{ m ITG}$	Y TAT	I ATA	A GCC	N AAT	P	A GCT
IGGA(CIC	Y TAT	S	G GGA	T H	P	M ATG
gagai	CIG	T ACC	CIC	C H G C	A GCC	G GGG	A GCA
3660	G GG	P CCA	A GCC	C Hec	P CCA	P	M ATG
3TCC(CIC	Y TAT	R CGG	F	E GAG	Q CAG	S TCC
CGGC	L	CHC	V GTG	CTT	E GAG	Q CAG	N AAT
SACC	L	G GGA	C TGT	V GTG	I ATC	A GCC	G GGG
CTGC	A GCG	E GAA	C HGC	9 GGC	L	G GGA	V GTC
3080	A GCG	H H H H C	R AGG	M ATG	P	P CCA	P
GCGAAGCGCCCTGCGACCCGGCGTCCGGG	V GTG	Y TAT	S TCC	M ATG	P CCG	G GGC	N AAC
7525	K AAG	W TGG	9 GGC	L	CCC	CCC	M ATG

Fig. 1A

FOTERET OTTOOT

166 632	173 653	732	811 890	696	1048	1127	1206	1285	1364	1443	1522	1601	1680	1759	1838	1917	1996	2075	2154
E GAA		CAG	ATGG STGT	CAG	AGG	TGL	TCT	;GGC	TCA	TTG	TGC	AAA	TGT.	AAC	TCA	TGA			
Y TAC		CTTC	TCC	AAGG	'TAA1	'AGCC	TCIG	ATG	GAAZ	TTT1	TCAC	TTTC	AGGI	ACTC	CAGC	GTGT	GCIG	GAAC	ATCG
PCCG		TTCA	GC'I''I CATG	GAAG	GTAI	CICC	TGTI	CAGG	ATGG	CCAI	GACA	GTGC	TCTG	ACIG	ATCA	TATA	ATGT	CATT	TTTA
CCC		GATG	TCAG	AGAG	SSSS	TCTG	GTCA	ACCG	ATTC	TTAC	CCTG	AAGG	TCTC	AAGT	AGGA	TAGT	CTAG	TACT	GACA
P		CGTT	TCLL	ACTG	CIGC	GTCA	CCLT	TCTC	\mathtt{TTAA}	ACTG	CTTC	TCTG	CGIC	GGAG	GGAT	CGCA	ATTA	TIGI	TGAG
PCCT		TCTT		AGAG	CCTT	GCAG	AGCC	CAGC	TTAT	AAGG	GTGT	GGGT	GAGG	GACA	TCCT	CCGC	CTAG	GAAA	ACTC
P P A Y C N T P P P P Y E CCT CCA GCC TAC TGC AAC ACG CCT CCG CCC CCG TAC GAA		TCTG	GCAG	GGAG	GCAT	CCCA	AGCA	CGTG	AAAT	GAGA	GTGT	TGGT	AGCT	AAAA	ACAT	AGTT	CCCC	\mathtt{TTGA}	TTTC
N AAC		CCTT	CAAG	TACA	GCAA	TGAG	AGAG	AGCA	AAGC	TTTG	CIGG	CCAG	GACC	TGGG	ATGC	AGCT	TGAG	CCIC	TGCT
C		CTGG	ACAG	GATC	CCAG	GAGC	CAGG	GGGT	CACT	CTGA	CAGA	AGCT	GAGA	TTGC	GGAA	9999	TAGC	AGAG	TCCA
Y TAC			TOL	ACCA	CATC	GACI	CATI	GGAA	CATC	'TGGT	AAAT	AGGC	GGGA	GAGC	CGIC	TAGC	AGCT	AATC	GGTG
A GCC		GCCI	TGCI	CGTG	CGAG	AGCC	GAGA	CCAG	CTGA	CICI	TITG	CCLC	TCCA	GGAG	AAGT	CGGC	ATGC	AACT	ATTT
P CCA		GAGG	CTGT	GTGG	'AGGC	CAGC	TGGA	ACCG	TGAT	TGAG	೧೧೧೮	CTTC	CICI	AGGA	GAAG	TTGA	AGCT	AATG	AGTG
CCT		AGGA	TCCI	'TACG	SEGCC	GAAG	CIGI	CIGC	ACAG	TITG	TCCI	TCTC	TGGA	TCCA	TAAA	GTAG	TAAG	TTTT	ACGG
	* TAG	AGAC	TGTC	TCCI	GAGG	CGAI	GAAG	TCIC	CCTG	GCAT	AGCG	99999	CACA	2999	AGAA	CTGA	GIGC	TATT	GGAT
P CCG	K AAG	4GGAG	ACTI	GACG	TGTA	CAGC	TCCA	GACI	GAGG	CATI	GTAG	೨೨೨೨	AAGI	TGCI	'AATT	TCIC	CIGI	TGCI	AAGI
TGC CCG	A GCC	AAAGA	TCAC	GGCI	GGCZ	GGCI	CTCI	GATA	CTTG	GAGA	GCAI	CAGG	TGGG	TGTG	TCAL	GTAG	TGIC	99999	ATGG
V A GTG GCC	K AAG	CGTGC	GAAC	CGAG	AGGI	GGGC	CTTC	TAA	TIGC	AAACI	AAGI	TICI	TGGC	3000	GTIG	ACAG	GACC	GGIG	TCIC
V GTG	V GTG	CCCAC	ATAI	STCCC	GIGC	\TGC(CAGC	'ATCC	AGGC	CCCF	ATG	GGCZ	CATC	TAAG	CCAI	TCIC	CGCI	ATGA	GACA
G S V A C P P 3GG AGT GTG GCC TGC CCG CCC	Q V V K A K *	TGGGGTGCCCACGTGCAAGAGAGAGAGAGAGAGGGGCCTTTCCCCTGGCCTTTCTGTCTTCGTTGATGTTCACTTCCAG	saaceelolooleeleecleclaaeecaelloololoolol	SGTGACAGTCCCCGAGGGCTGACGTCCTTACGGTGGCGTGACCAGATCTACAGGAGAGAGA	IGCTGGAGGTGCAGGTGGCATGTAGAGGGGCCCAGGCCGAGCATCCCAGGCAAGCATCCTTCTGCCCGGGTATTAATAGG	AAGCCCCATGCCGGCCGCTCAGCCGATGAAGCAGCAGCCGACTGAGCTGAGCCCAGCAGGTCATCTGCTCCAGCCTGT	CCTCTCGTCAGCCTTCCTCCAGAAGCTGTTGGAGAGACATTCAGGAGAGAGA	TGTTCATATCCTAAAGATAGACTTCTCCTGCACGCCAGGGAAGGGTAGCACGTGCAGCTCTCACCGCAGGATGGGGC	TAGAATCAGGCTTGCCTTGGAGGCCTGACAGTGATCTGACATCCACTAAGCAAATTTATTT	TICCTGCCCCAAACTGAGACATTGCATTTTGTGAGCTCTTGGTCTGATTTGGAGAAAGGACTGTTACCCATTTTTTGG	TGTGTTTATGGAAGTGCATGTAGAGCGTCCTGCCCTTTGAAATCAGACTGGGTGTGTGT	TCTCCAGGGCATTCTCAGGCCCGGGGGTCTCCTTCCCTCAGGCAGCTCCAGTGGTGGGTTCTGAAGGGTGCTTTCAAA	ACGGGGCACATCTGGCTGGGAAGTCACATGGACTCTTCCAGGGAGAGAGA	STIGGGICTAAGCGGGIGIGIGCIGGGCICCAAGGAGGAGGAGCIIGCIGGGAAAAAAAA	FGCACTGACCATGTTGTCATAATTAGAATAAAGAAGAAGTGGTCGGAAATGCACATTCCTGGATAGGAATCACAGCTCA	CCCCAGGATCTCACAGGTAGTCTCCTGAGTAGTTGACGGCTAGCGGGGGGGG	FGTGTGAACGCTGACCTGTCCTGTGTGCTAAGAGCTATGCAGCTTAGCTGAGGCGCCCTAGATTACTAGATGTGTGTATAT	CACGGGGAATGAGGTGGGGGGTGCTTATTTTAATGAACTAATCAGAGCCTCTTGAGAAATTGTTACTCATTGAACTGG	AGCATCAAGACATCTCATGGAAGTGGATACGGAGTGATTTGGTGTCCATGCTTTTCACTCTGAGGACATTTAATCGGAG
G.G.G	Q CAG	TGGC	AGT?	3GT(IGC1	AAGC	CTC	CIGI	CTAC	CTTC	GTG1	CICI	ACGC	3TTC	rgcz	2222	rgre	CACC	4GCZ

Fig. 1E

2707 AACCTCCTGGGGAATTTTGTGGGAGACACTTGGGAACAAAACAGACACCTGGGAATGCAGTTGCAAGCACAGATGCTG TGAGACAACAAAGCACAATGTTCACTGTTTACAACCAAGACAACTGCGTGGGTCCAAACACTCCTCTTCCTCCAGGTCA TTTGTTTTGCATTTTTAATGTCTTTATTTTTTGTAATGAAAAGCACACTAAGCTGCCCCTGGAATCGGGTGCAGCTGA ATAGGCACCCAAAAGTCCGTGACTAAATTTCGTTTTGTCTTTTTGATAGCAAATTATGTTAAGAGACAGTGATGGCTAGG GAACGCTGATCCTGCATATGGAAGTCCCACTTTGGTGACATTTCCTGGCCATTCTTGTTTCCATTGTGTGGTGGT CCACCAGTGTCTCTGACCACCCTGGTGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGCTGCAGGCCTCCATCTAAA TTGTGCCCACTTCCTGGAGTGAGACAGCTCCTGGTGTGTAGAATTCCCGGAGCGTCCGTGGTTCAGAGTAAACTTGAAG CAGAICIGIGCAIGCITITCCICIGCAACAAIIGGCICGIITICICITITITIGIICITITITGAIAGGAICCIGIITICCI AAAAAAAAGGGCGGCCGC

Fig. 1C

151 V A A L L G L L V E C T E A K K H GTG GCG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCCTCGCTGGAGCC ATG GGC CGC CGG CTC

Fig. 1D

45	271
ರ	IGC
Ω	GAC
臼	GAA
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ഗ	TCC
ĸ	CGT
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Д	CCC
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Ы	CIC
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曰	GAA
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M	$^{ m LGG}$
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165	631
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Н	CAC

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\triangleright	GIG
Oĭ	CAG
ഥ	GAA

CAAGATGCTACATCAAAGGCAAAGAGGATGGACAGGCCCTTTTGTTTACCTTCCCATCCTCACCGATACTTGCTGATAG 734

Fig. 1E

1366 1208 1287 1445 1524 1603 1682 1761 1840 1919 1998 2156 2235 2314 2393 2077 2472 GGTGGTCCAAGGGAAAACTTGGATATTCTCAAAGCAAGCCCAGCTCTCTTTCAAGTCTTTTGTGGAGGACATTTGAATC CACACTGTCTCCTCTGTTGCTTCTGTTTCTGATGTAGTCTGTGCTCTCTGAGAGAGTGTGTGGCAACAGTCCCTGAGGGTT CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACTTCGAAGAGAGACACTATCCACCA TCCCAGCCCATTCTCCTAATAGAAGCTGTGGGGCTGTGTTGTTGATGCTCTTTGGTCTCCACTCACATTTTGAAAATAG GCTTTCCTCTGCAGGAATAGGAAAGACCCAAGTACATATTTGCTTCCACTTAAAAATGAGGGTCAGAACCAGGCCTCAG TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATTCTCTAAATGGAGAGACATT GCGTTTTATGAATCATCGTCTGGCTTTTTTTTTAGTGCATGTATTGAAGTGAGGGTGTCCTTTGAGATCAGATGGGGAG AGTGAACTCTGCGGGGGGGGGGGTGTCTCTACTCAGAGGGCTCCAACACCCTTTTCTTAGGTAGTTCTGGTGATGGGTT TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTGACCCTTGGAGAGGAAGAGGACAGCCAAAG AAACTCAGCAAAGCAAGACCAGCATTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGGCCTCA TGTAGTTAGAGATGCCATTTCCCCAGGTGAGAATCAGAGCTCATCCATAGATTTACAAGTAGTGGCTGGAGTTAACAGTA TGGAGTICTTTTCCCTTGCGTAGTTAGTCACGTTGATGTGTATTTAAACCCCAGGTTGAGACCTTGTGTATAAGAGCAA GAGTATTCTTTACCACCTACAAGACCAGGAGGCATGGTGTCATTCTCCATTGGGGGTATTTATATGAGGTAGTTCAG GAATCGACAGTAGCTGTGTGGGCTTAGTTTAAGGACTGAAAGCATAGGGACTGGTAGACAGTTTCATAGGAAACTGCGG TAAATGAGAAAATCAGAGCCATTTGATAAACTGTTACTTGTTGGATCAGGCATCCAAAAGTGTCTCTTGAGTGGACATT GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTGAGCACCCTTGTGTCTCTGGG CAATGTCTGTGTAAGGTAAATTTTGTTTGCCATTGAGCCCCACATTGGAATTCCTTCTGACGTCAACACTGACAATGCCT TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGGTCCTTGTTTTACATAAGACAACAAGACAAAGGTCTGCTGTTTT TACAATCAAGACGACTACATGGTCCAAACATTTCTTCTTCTTTTTAACTTGTGGCTTTAACTTCCATTTCCTCCGTT CCTTTTTAAAATCAAGAAGCACAGTCAGAGCTGCCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGTC CATGACTAAATCTTATCTTTTGATAGCAAATCCTTTTAAGAAACTGAACAATTGCTAAGGCTCAGCAATTTATACTC ATGGAAATTGCACTTCTGGGTATATGTCCCAGCATCCTTGTTTTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC

2788 2867 AGCTCTACTTCTGTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCCACAGACATGAGGCAGACTTGTGCATGCTCTTTC

Fig. 1G

Fig. 1H

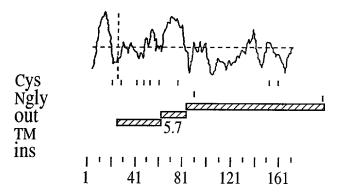


Fig. II

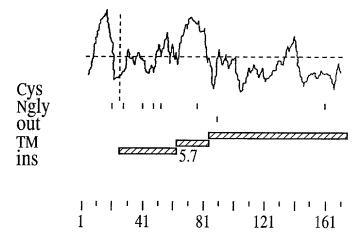


Fig. 1J

79	6	26 212	46	66 332	86 392	106 452	126 512
AATA	F	H CAC	C Hec	Y TAT	CII	Q CAA	G GGA
raa <i>ti</i>	Q CAG	CIC	N AAC	CIG	S TCT	V GTT	P CCT
TTCAGATTTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATA	$_{ m TTA}$	L TTA	I ATT	F TTT	H CAT	F	D GAT
CTGA(G GGA	$_{ m L}$	Q CAA	V GTT	L	A GCC	$_{ m L}$
rcag($_{\rm TGT}^{\rm C}$	$_{ m TTA}$	R AGA	T ACA	G GGA	K AAA	R CGC
rgaa.	M ATG	L	GGG	S AGT	T ACA	P CCA	K AAA
TTAC	GGAT	Y TAT	T ACT	E GAA	L TTA	Y TAT	I ATC
ACCT	ACAG($_{\rm TGT}^{\rm C}$	C	P CCT	E GAA	V GTA	H H H C
GAAA	AAGA	T ACC	L	F TTT	S AGT	Y TAT	N AAT
AAAA	TGAACAGAAATCCAAGAACAGGGAT	V GTT	Q CAG	N AAT	E GAA	Γ	N AAT
TTTA	GAAA	V GTT	C TGT	K AAG	N AAT	I ATT	N AAT
CAGA	AACA	L	V GTT	P CCT	I ATA	N AAC	L CTA
TCIL	TCTG	F TTT	S TCT	I ATT	Y TAT	S TCT	FTT
TCGT	CTGA	L CTG	S TCG	S AGT	S	N AAT	$_{ m CTA}$
AATG	AATT	R CGA	C TGT	S TCG	I ATA	D GAT	FL
CGGA	TGCC	L CTA	G	CTT	N AAT	TIG	Y TAT
CGTC	TTCT	C TGC	L	U U U	N AAT	Y TAT	$_{ m CTA}$
CACG	CCIT	PCCT	I ATA	L TTA	GGG	L TTG	H CAT
GTCGACCCACGCGTCCGGAAATGTCGTTC	CGAATTTCCTTGCCAATTCTGATC	L	E GAA	N AAC	T ACT	A GCA	R AGG
GIC	CGA	S TCT	K AAA	R CGT	L	V GTA	L TTG

Fig. 2A

146 572	166 632	186 692	206	226 812	246 872	266 932	286 992
F	N AAT	D GAT	L	V GTA	T T T	N AAT	N AAT
S T T	R AGG	CTT	N AAC	E GAA	CCC	R AGG	H CAT
V GTA	Q CAA	I ATA	E GAA	F	Q CAG	I ATT	s AGT
Q CAG	$_{ m CTA}$	R CGG	L	A GCC	I ATA	R AGA	L TTA
N AAT	N AAT	CTT	H CAT	N AAT	A GCA	S TCA	I ATC
Y TAT	L TTA	A GCT	Q CAA	S TCA	E GAA	N AAT	TT C
Q CAG	$^{ m Y}$	V GTT	F TTT	P CCA	I ATT	K AAA	H CAT
$_{ m L}$	Q CAG	M ATG	G GGC	V GTA	PCCT	L	K AAA
Y TAT	V GTT	G GGT	S TCA	K AAA	N AAT	CIC	L
$_{ m TTA}$	S TCA	V GTT	E GAA	T ACA	H CAT	CIC	N AAT
N AAT	V GTT	T T T T	S TCA	L TTA	S TCT	$^{ m Y}_{ m TAC}$	N AAT
RCGT	$_{ m CTA}$	TACC	I ATA	N AAT	Γ	E GAA	I ATT
L	D GAT	GGT	R AGG	N AAT	S TCT	CIG	G GGA
N AAT	N AAT	S AGT	L TIG	S AGT	CHI	N AAT	S AGT
L TTA	H H H H H	GGG	I ATT	G GGA	R AGA	A GCC	F
CTT	V GTA	CIT	N AAC	L TTA	R AGA	CIT	G GGG
GGA	G GGA	V GTC	N AAT	Y TAT	L	G GGA	D GAT
K AAG	R AGA	T ACT	N AAC	L TTG	S AGT	K AAA	R AGG
H H H H H H	P	L	S TCA	C H CH	K AAA	F	T ACT
I ATA	V GTT	R CGC	L TTA	A GCT	CII	A GCA	VGTT

Fig. 2B

306	326	346	366	386	406	426	446
1052	1112	1172	1232	1292	1352	1412	1472
K	S	K	K	Q	T	K	N
AAG		AAG	AAA	CAG	ACA	AAG	AAT
L	A GCA	L	C HGC	$^{\mathrm{TGT}}$	V GTT	H CAC	E GAA
YTAC	G	V	N	Y	C	H	L
	GGA	GTC	AAC	TAT	TGT	CAT	CTG
I	M	R	C	I	N	I	P
ATT	ATG	AGG	TGT	ATC	AAT	ATT	CCT
L	N	P	E	N	T	H	S
TTA	AAT	CCA	GAA	AAC	ACA	CAT	AGT
N	E	H	W	L	I	P	g
AAT	GAA	CAT	TGG	CTA	ATT	CCT	GGC
K AAG	다 단 단	L TTG	P CCT	T ACT	N AAC	S TCT	N AAT
L	T	A	N	I	I	K	T
TTA	ACA	GCC	AAT	ATT	ATT	AAA	ACA
L	D	T	S	A	Y	V	T
TTG	GAT	ACA	TCT	GCC	TAT	GTA	ACC
S	N	L	N	S	R	V	V
AGT	AAT		AAT	TCA	CGT	GTT	GTA
T E	D	N	A	S	L	A	K
	GAT	AAT	GCA	TCT	TTA	GCT	AAA
T	I	N	Q	A	A	W	H
ACA	ATT	AAT	CAG	GCA	GCA	TGG	CAT
D GAC	S AGC	F	L	L CTA	R AGA	A GCT	\overline{W}
S TCT	I ATT	S TCA	H CAT	WTGG	9 9 9 0	R AGA	A GCC
N	I	CIG	I	D	R	S	M
AAT	ATA		ATT	GAC	CGT	TCC	ATG
L	R	N	L	R	M	V	M
TTA	AGA	AAT	TTG	CGA	ATG	GTA	ATG
N AAT	N AAC	L	S TCA	CTT	S TCC	N AAT	L CTA
E GAG	R AGA	I ATC	S TCT	G G G	P CCA	I ATA	A GCG
L TTA	D GAT	K AAG	I I G	Γ	CCC	S TCA	T ACT
D GAT	L TTA	L TTG	Р ССG	CII	N AAT	S TCT	TACT

Fig. 2C

486 1592 506 1652 466 532 526 1712 566 1832 546 772 586 892 606 952 F TTT I ATA A GCT E GAG I ATC R AGA N AAC I ATT Q CAA AGA D GAT N AAT $\stackrel{\text{L}}{\text{TTG}}$ N AAT $_{\rm TGT}^{\rm C}$ CAA \circ GGT V GTG N AAT Γ E GAA F TTT I ATT K AAA ᢗ PCCT PCCG K AAG I ATT R AGG S TCA H CAT ℧ $_{\rm L}^{\rm L}$ GAG CCT L CTA I ATC S TCA A GCC LCTT Д ഥ S TCA V GTG A GCT V GTT L TTA N AAC T ACT R CGA A GCA ACT S AGT E GAA E GAA V GTT VGTA I ATT \vdash CCT T ACA N AAC Q CAA $_{\rm TGT}^{\rm C}$ S TCA CAG N AAT \circ T ACT I ATT K AAA T ACA A GCT A GCA TAT E GAG \succ R CGA E GAG E GAA CTGT L TTA K AAG R AGG $_{
m L}$ E GAA Γ L TTA I ATT I ATC L CTA GCA GGC Ø IGG P CCA N AAC L CTA $_{\rm TTC}^{\rm F}$ K AAA S TCA PCCT TIC Γ N AAT STCT F TTT Q CAA Q CAG S AGT ഥ GGT TACC ACA GAA A GCT K AAA TAT Ħ \succ ഥ I ATT FTTT GTT K AAA L CTA L CTA F TTT F TTT \gt AAC GGG A GCC S TCT $_{
m L}$ Q CAG AGC STCT S E GAG N AAT T ACT S TCA I ATT V GTT TAC N AAT \succ T ACT EGAG D GAC TACT V GTT YTAC CCA \sum Д E GAG Q CAA LCTT S TCA FTT K AAA GAA S TCC 囗 TACT F TTT Q CAA A GCT A GCT T ACT Y TAC LCTT

Fig. 2D

\triangleright	V P	闰	Z	日	A	Ø	\triangleright	V I L F	Ц	ഥ	曰	H	യ	Ø	H S A L	*		623
GTT	CCI	GAA	AAT	GAG	GTT CCT GAA AAT GAG GCA CAG		GTC ATT CTT TTT GAA CAT TCT GCT TTA TAA	ATT	CLI	TII	GAA	CAT	\mathtt{ICT}	CCT	${ m TTA}$	TAA		2003
CIC!	AACTE	AAATE	ATTGI	ICTA	TAAG?	AAACI	rtcag	TGCC	ATGG	ACAT	GATT	TAAA	CTGZ	AAACC	TCCI	CTCAACTAAATATTGTCTATAAGAAACTTCAGTGCCATGGACATGATTTAAACTGAAACCTCCTTATATAATTATATAC	ATATAC	2082
${ m TT}$	\GTT6	GAAZ	TAT!	AATG2	AATT?	ATATC	BAGGI	'TAGC	ATTA	TTAA	AATA	TGTT	TLL	ATAZ	AAAA	TTTAGTTGGAAATATAATGAATTATATGAGGTTAGCATTATTAAAATATGTTTTTAATAAAAAAAA	AAAAGG	2161
BCG	25225525	<i>T</i> \																2169

Fig. 2F

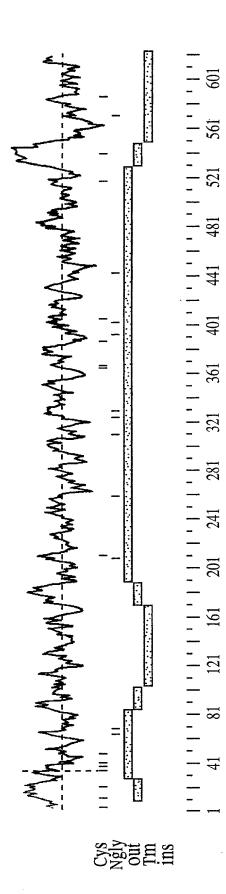


FIG. 25

COPESTA DATOO

ს ს	⊢l I	[[]	0, 1
DLN ::	RLD ::: RLD	LRT.	LHC
60 FERL: :	130 AKLYI • • • 120	200 IMPK	270 CSV
PRN: PES:	LLFLGTA .::: FLFLNNN	S ENF	4APS
RNI KNF	H • H T • H	SVAS	OS 1
50 38VP 381P	120 130 LQLFPELLFLGTAKLYRLDL .::: ::: -HLYFLFLNNNFIKRLD- 110	190 IITRL: :: : LTVL(260 SSGH(
20 30 40 50 60 VLAILNKVAPQACPAQCS-CSGSTVDCHGLALRSVPRNIPRNTERLDLNG ::.: .:.:: :::::::::::::::::::::::	HLQL .: HL	150 160 170 180 190 KAFRGAVDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASF :::::::::::::::::::::::::::::::::::	E FV(
))CHG .:	O INRN	TLN:) 70kr
40 STVD 	110 RLRLI	180)LEVL; : .VQYL]	250 HNVAEV(:: VA
-CSG : :	(E1.E	ALRD:	GHNV.:
OCS- : VCQI	O QDLK .:. VQLF	O AFRA .:.	SHLR
30 ACPA	100 (GAFQI :: %KAFV(170 EDGA:	240 MGPS:
APQA • EILC 30	TIEF YVYE 100	ISCI .:. VSFV	YTOC
	90 NKIS SNIL	ONY()	230 PRVGLY ::. VGM-
20 IL	90 LMENKI :: LDNSNI	160 LQLDYI : ::: LYLQYI 140	230 2RPRV(:
 CYL.	LRVLQL : .: : LVALYL 90	J KN:	WLR(
LVL? :: LVVI	80 RHLF . : HSLV	50 GAVE : GLLN	ZO WLSD
SLG	TDFAGL: SELTGL: 80	15(AFRG)	22(HLAWI:
10 MLSI . : LPCI	KTDE.	I : I : I : I : I : I : I : I : I : I :	YCDC
GWQI	70 'RIT] :.	140 QIQAIP : PGI-	210 SNNL
10 MRGVGWQMLSLSLGL : : : : : : : : : : : : : : : : : : :	NNITR:::.	140 150 160 170 180 200 SENQIQAIPRKAFRGAVDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASFNHMPKLRTF: ::::::::::::::::::::::::::::::::::	210 220 230 240 250 260 270 RLHSNNLYCDCHLAWLSDWLRQRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSGHQSFMAPSCSVLHCP ::VAVA
10 Slit MRGVGWQMLSLSLGLVLA ::::::::::::::::::::::::::::::::::	70 80 100 110 120 130 Slit NNITRITKTDFAGLRHLRVLQLMENKISTIERGAFQDLKELERLRLNRNHLQLFPELLFLGTAKLYRLDL :::::::::::::::::::::::::::::::::::	Slit 325	Slit] 325 ·
Ω (.)	Ω	Ω (,)	\mathbb{S}

Fig. 20

280 330 340 AACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQNTIKVIPPGAFSPYKKLRRIDLSNNQISELAPDAF :::::::	0 370 380 390 400 410 ITELPKSLFEGLFSLQLLLLNANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKG ::: ISE	420 430 440 450 460 470 480 TFSPLRAIQTMHLAQNPFICDCHLKWLADYLHTNPIETSGARCTSPRRLANKRIGQIKSKKFRCSAKEQY :: :: 210) 510 520 530 540 550 CFADLACPEKCRCEGTTVDCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIF .:.: .: .: .: .: .: .: .: .: .:
280 300 300 31 Slit AACTCSNNIVDCRGKGLTEIPTNLPETITEIRLE	350 360 370 38 Slit QGLRSLNSLVLYGNKITELPKSLFEGLFSLQLLL] :: ::325LRISE	420 430 440 45 Slit TFSPLRAIQTMHLAQNPFICDCHLKWLADYLHTNP :: : 325YLGSN-	490 500 510 52 Slit FIPGTEDYRSKLSGDCFADLACPEKCRCEGTTVDC

Fig. 2H

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Fig. 2]

840 850 860 870 880 890 900 GNDISVVPEGAFNDLSALSHLAIGANPLYCDCNMQWLSDWVKSEYKEPGIARCAGPGEMADKLLTTPSK ::::::::::::::::::::::::::::::::::::	0 930 940 950 960 970 NPCLSNPCKNDGTCNSDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCH : : : : : : : : : : : : : : : : : : :	0 1000 1010 1020 1030 1040 FEGENCEVNVDDCEDNDCENNSTCVDGINNYTCLCPPEYTGELCEEKLDFCAQD :::	0 1070 1080 1090 1100 1110 FKCDCTPGYVGEHCDIDFDDCQDNKCKNGAHCTDAVNGYTCICPEGYSGLFCEF : :
890 IARCAGPGEM	960 DCDVPIHACI : : -CQNP	1030 CCPPEYTGEL	1100 TDAVNGYTCIC:: TSSIN
880 WVKSEYKEPG: :	950 TCPYGFKGQI	1020 CVDGINNYTCI	1090 IKCKNGAHCTI :-
0 860 870 ALSHLAIGANPLYCDCNMQWLSDWVKS: :::::::::::::::::::::::::::::::::::	940 CNSDPVDFYRC : Y	1010 EDNDCENNSTCVD ::: NITNCV-	1080 EDIDFDDCQDN
860 HLAIGANPLYC :: .:: ; HLQANSNPWEC	930 SNPCKNDGTC	1000 INCEVNVDDCE	1070 CTPGYVGEHC
850 AFNDLSALSF :::::	920 NILAKCNPCI :: NI	990 CICADGFEGE :	1060 ILTPKGFKCD
840 GNDISVVPEG?	910 92 KFTCQGPVDVNILAKCI ::	980 LKEGEEDGFWCICADG	1050 106 LNPCQHDSKCILTPKG
slit 325	Slit 325	Slit 325	Slit 325

Fig. 2.

DOYMENT DITONI

1120 1130 1140 1150 1160 1170 1180 t SPPMVLPRTSPCDNFDCQNGAQCIVRINEPICQCLPGYQGEKCEKLVSVNFINKESYLQIPSAKVRPQTN .:: .: .: .: .: .: .: .: .: .: .: .: .:	1190 1200 1210 1220 1230 1240 1250 t ITLQIATDEDSGILLYKGDKDHIAVELYRGRVRASYDTGSHPASAIYSVETINDGNFHIVELLALDQSLS :: : : : : : : : : : : : : : : : : : :	1260 1270 1280 1290 1300 1310 1320 t LSVDGGNPKIITNLSKQSTLNFDSPLYVGGMPGKSNVASLRQAPGQNGTSFHGCIRNLYINSELQDFQKV :: :: :: :: :: :: :: :: :: :: :: :: ::	1330 1340 1350 1360 1370 1380 1390 t PMQTGILPGCEPCHKKVCAHGTCQPSSQAGFTCECQEGWMGPLCDQRTNDPCLGNKCVHGTCLPINAFSY .:: :
	1190 Slit ITLQIATDEI 325TTNGS	<u>ე</u>	1330 Slit PMQTGILPGC .:: . 325 NEAFDILLA-

Fig. 2K

1400 1410 1420 1430 1440 1450 1460 Slit SCKCLEGHGGVLCDEEEDLFNPCQAIKCKHGKCRLSGLGQPYCECSSGYTGDSCDREISCRGERIRDYYQ	SENSRENRL-EYY- 560 570	CGCTRCVS	· · -LFEHSAL 620
1450 rgdscdreise	SENS560	1520 VDEVEKVVKO	.: :
1440 PYCECSSGY1	 	1510 SFECTDGSSI	1
1430 GKCRLSGLGÇ	IIFLIYKVVQFKQKLKA 550	1500 GPLRSKRRKY	SPNSLESPGLEQIRLHK-
1420 NPCQAIKCKH	LIYKVVQFKQKLKA 550	1490 RGGCAGGQCC	 NTSPNSLESP 590
1410 VLCDEEEDLE	! ! 凸	1480 FK-KVSRLEC	ARYNVTASIC 580
1400 SCKCLEGHGG	325 ACV 540	1470 1480 1490 1500 1510 1520 Slit KQQGYAACQTTK-KVSRLECRGGCAGGQCCGPLRSKRRYSFECTDGSSFVDEVEKVVKCGCTRCVS	325SFYQSARYNVTASICNTSPNSLESPGLEQIRLHK 580 590 600
Slit	325	Slit	325

Fig. 2L

		20	30	40	50	09	70
S. L. C.	SIIT CAGAGCAGGGTGGAGGGCGGTGGGAGGCGTGTGCCTGAGTGGGCTCTACTGCTTGTTCCATATTATT	AGGGCGGTGGGA	reecereracc	TGAGTGGGCT	CTACTGCCTT	'GT'I'CCAT'AT'I'	
373		 	! ! ! ! ! !			 	
Slit	80 TTGTGCACATTTTCC	90 140 110 120 130 140 CTGGCGGCCACTGGGCCTCAGACACTGCGCGGGTTGCTAGCCCGGGGCACTGGGCCTCAGACACTGCGCGGTTGCTGCGCGGTTGCTGCGCGGGTTGCTGGGCCTCAGACACTGCGCGGTTGCTGGGCCTCAGACACTGCGCGGTTGCTGGGCCTCAGACACTGCGCGGGTTGCTAGCCCGCGGGCACTGGGGCCTCAGACACTGCGCGGTTGCTAGACACTGCGCGGTTGCTAGACACTGCGCCGGGCTTGGGCCTCAGACACTGCGCCGGGCTTGCGGCCTCAGACACTGCGCCGGTTGCTAGACACTGCGCCGGGCTTGCTAGACACTGCGCCGGGCCTCAGACACTGCGCCGGCCTCAGACACTGCCCGCCGGTTGCTAGACACTGCGCCGCGGCCACTGCGCCTCAGACACTGCCCGCCGCGCTTAGACACTGCCCGCCGCGCCACTGCGCCTCAGACACTGCCCCGCCGCCGCCGCCACTGCCCCGCCGCCGCCGCCACTGCCCCCGCCGCCACTGCCCCCGCCCG	100 GTTGCTAGCC	110 cccccccc	120 CTGGGCCTCA	130 AGACACTGCGC	140 GGT
325							1
	ر د د	C F	7	α 7-	0		010
Slit	ICCCICG	AGCTAAAGAAAG	CCCCAGIGC	CGGCGAGGAA	GGAGGCGGCG	GGGAAAGATG	0 C C C C C C C C C C C C C C C C C C C
325							!
	C	C C	C 70	C C	C		C
Slit	GGCGTTGGCTGGCAGATGCTGTCCCTGTGGGGTTAGTGCTGGCGATCCTGAACAAGGTGGCACCGC	ZSU ATGCTGTCCCTG	ZYU TCGCTGGGGT	230 'TAGTGCTGGC	280 GATCCTGAAC	, AAGGTGGCAC	7 ° 0 CGC
		••	••			••	
325		9	-GTCG			ACC-	

Fig. 2M-1

350 AGCGT :::	420 ACGAAG	490 TGAAA :.	560 TGTTTCC ::::
290 340 350 Slit AGGCGTGCCCGGCCAGTGCTCTGGGCAGCACAGTGGACTGTCACGGGCTGGCGCTGCGCAGCGT ::: 325CACGCGT	370 380 390 400 410 420 CGCAACACCGAGAGATTTAAATGGAAATAACATCACAAGAATTACGAAG	440 450 460 470 480 490 TTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAA ::::::::::::::::::::::::::::::::	510 520 530 540 550 560 ICTTAAAGAACTAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCC :: ::::: ::: .:: .:: .:::::::::::::::
330 TCACGGGCTG :::: -CACG	400 ATAACATCA 	470 GAATAAGAT :.: AGAAAA	540 AGAAATCAC :::. AATACG- 80
GGACTGTC	AATGGAA?	470 TTATGGAGAATA :::.: TTTAAAAAGAAA	TTTAAAC?:::-
320 AGCACAGT	390 TGGATTTA	460 470 GTTCTTCAGCTTATGGAGAATAA ::::::::::::::::::::::::::	530 AGACTGCG' : TG
310 GCTCGGGC	380 CGAGAGAC	450 CTAAGAGT ::	520 GAACTAGAGAGA :.:::::-: -AGCT-GAGTG-
300 AGTGCTCTT	370 3CGCAACAC		510 ATCTTAAAG ::: ATC
290 ccceecec	360 GCCCAGGAATATCCCC ::::::: CCGGAATGTC	430 ACAGATTTTGCTGGTC	500 GAGGAGCATTCCAGGA :.:.:
AGGCGTG			
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 2M-2

630 ATC	!	700 GTA ::- GTT 50	770 TAG	840 GTAT :: AT
6 CAA]	7 T C T C T C T C T C T C T C T C T C T	4CI	84 IGTA' : : A' 200
	ပ္ ပ္	AG(I_{LL}	CC1
CA::	130 130	E I	CA.	AA.
620 AATT	3A.B	690 CAGA	760 ACAA	830 AAAC
62 AAZ	AA(722	7 (AA(CAZ
620 AAAACCAAATTCA	-ACAGA-AAATCCAAGAACAGG- 120 130	650 660 700 680 690 700 CGTGGGGCAGTTGACATTTGCAACTGGATTACAACCAGATCAGCTGTA .:.: :: :: :: :: :: :: :: :: :: :: :: ::	 	T.T.
AAA	AAT(120	680 ACTGGATTACA :::::::	0 CAACAA:::: CTACGA: 170	GCP
O GAZ	A	0 'AT' ::	CAN CTI	CTC
610 TCAGTG	4GA	680 TGGA' TGGA'	750 lcTC :	820 3GAC
TCZ	AC/	ACT: T	AC.) H •• H
TC		CA	D I	ACTTTT .:::: TCTTTT
0 TG2	 	670 AAAAATTTG ::::::	40 GTGC' -::: -TGC	0 GAC - TC
600 3CTT	 -	670 AATT ::	740 \AGT(810 'AGG
AGG	CTGF 110	6' AAAA' GATA'	. i	CIJ
90 CTATACAGG	LIC 1	'AA'	0 GACCTG .::: -GCCT- 160	
D IAT	I'GA	CAI	0 3ACC' .:: -GCC'	0 D I
590 GCT	J L	660 GAC	730	800 GCC
CGAA	CAAT 100	T T T		TAT TTS
255	-C7	CA(CATJ :. CTG'
CI.	ပ္	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1) · · · · · · · · · · · · · · · · · · ·) \AC \::
580 GGA	 	650 TGG	720 AGG	790 ICA GII
Д	D I		J. I.	
ICI	ICI I		CAT	AAG. : TGG. 180
H ••	-TTTCTTGCCAATTCTGATCTGA- 90 110	L C	<u>.</u>	
570 CTG	1 0	640 CCAAGGAAAGCTTTC	710 TGG(780 810 820 840 ACTITCTGTGGCAAGTTTCAACCATATGCCTAAACTTAGGACTTTTCGACTGCATTCAAACAACTGTAT :::::::::::::::::::::::::::::::::
TG(GAZ	.GA!	7 (CTG)
4GT		1AG	3AB	
570 580 600 600 610 620 630 1GAGTTGCTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	i ⊟	CC!	710 720 730 740 750 760 770 170 170 170 170 170 170 170 170 17	AC.
	325	lit 325	Slit 325	Slit 325
Slit	m	slit 325	31. 3%	33.

Fig. 2M-3

850 860 910 IGTGACTGCCACCTGGCTCTCCGACTGGCTTCGCCAAAGGCCTCGGGTTGGTCTGTACACTCAGT ::::::::::::::::::::::::::::::::::::	920 930 940 950 960 970 980 GTATGGGGCCCTCCCACCTGAGGGCCATAATGTAGCCGAGGTTCAAAAACGAGAATTTGTCTGCAGTGG ::::::::::::::::::::::::::::::::::	990 1000 1010 1020 1030 1040 1050 TCACCAGTCATTTATGGCTCCTTGTAGTGTTTTTGCACTGCCGCCTGTACCTGTAGCAACAAT ::::::::::::::::::::::::::::::::	1060 1070 1080 1090 1110 1110 1120 ATCGTAGACTGTGGGAAAGGTCTCACTGAGATCCCCACAAATCTTCCAGAGACCATCACAGAAATAC :::::::::::::::::::::::::::::::::
850 Slit TGTGACTGCC ::::::::	920 Slit GTATGGGCCC :::: 325 GTTTG	990 Slit TCACCAGTC?::::	1060 Slit ATCGTAGACT :: 325CT

Fig. 2M-4

1130 1140 1150 1160 1170 1180 1190 GTTTGGAACACACAATCAAAGTCATCCCTCCTGGAGCTTTCTCACCATATAAAAAGCTTAGACGAAT :::::::::::::::::::::::::::::::::::	1200 1210 1220 1230 1240 1250 1260 TGACCTGAGCAATAATCAGATCTTCTGAACTTGCACCAGGACTACGCTCTCTGAATTCA :::: TAACAGGACTTCATTCT	1270 1280 1300 1310 1320 1330 CITGTCCTCTATGGAAATAAAATCACAGAACTTCCCCCAAAAGTTTATTTGAAGGACTGTTTTCCTTACAGC ::::: CTTGTAGCAGCATTGTATTTGGATAATTCTAACA 400 410 420	1340 1350 1360 1370 1380 1390 1400 TCCTATTATTGAATGCCAACAGATAAACTGCCTTCGGGTAGATGCTTTTCAGGATCTCCACAACTTGAA : ::::::::::::::::::::::::::::::::::
1170 11 TTCTCACCATATAAAAA:::::::::::::::::::::::::::	1240 CTTTCCAAGGACTACG ::::::	00 1310 AAGTTTATTTGAAGGAC' : ::::::	1380 GATGCTTTTCAGGA' : :: :: TTCAATTGAGG450
1160 rccrggagcritc :::::	1230 3CACCAGATG	1300 TCCCCAAAAGT : : ATT	0 1370 TGCCTTCGGGTA ::::: :
1150 AAGTCATCCC	1220 CTCTGAACTT	1290 ATCACAGAACT :: AGC-	1360 AGATAAACTG : G
1140 AACACAATCA : A	1210 ATAATCAGAT 	1280 TGGAAATAAA	1350 AATGCCAACA :::::::: TAT-CCAAAA
1130 Slit GTTTGGAACAGA :::::: 325TGTATCTGA	1200 Slit TGACCTGAGCA :.:: 325 TAAC	1270 Slit CTTGTCCTCTA :::: 325 CTTGT	1340 1350 Slit TCCTATTATTGAATGCCAACAA : :::: :::: : :::: : TTCTGTATGTATAT-CCAAAA- 430 440

Fig. 2M-5

0 H H	0 0 0	0 U H 0	0 I
147(CCAT	1540 rcrcc ::: :	1610 ATTGG : TATTT 550	1680 ATTAT
1410 1420 1430 1440 1450 1460 1470 CCTTCTCTCCCTATATGACAAGCTTCAGACCATCGCCCAAGGGGACCTTTTCACCTCTTCGGGCCATT ::::::::::::::::::::::::::::::::::	1480 1490 1500 1510 1520 1530 1540 CAAACTATGCATTTGGCCCAGAACCCCTTTATTTGTGACTGCCATCTCCAAGTGGCTAGCGGATTATCTCC ::::::::::::::::::::::::::::::	1560 1570 1580 1590 1600 1610 AGACCAGTGCCCGTTGCACCAGCCCCCGCCGCCTGGCAACAAAAAATTTGG : : : : : : : : : : : : : : : : : :	1630 1640 1650 1660 1670 1680 GAAATTCCGTTGTTCAGCTAAAGAACAGTATTTCATTCCAGGTACAGAAGATTAT :::::::::::::::::::::::::::::
09 I	30 CGGAT	00 CAAA AI	70 ACAG
1460 CCTCT	1530 TAGCG(::	1600 ZAAACAJ	1670 AGGTAC
TTTCA ::::: TTTCA 490	20 AAGTGGCTA ::::::::	TGGC	TCCZ
1450 ACCTT	1520 15 :TCAAGTGGCTAG ::::::::	1590 CCGCC	1630 1640 1650 1660 GAAATTCCGTTGTTCAGCTAAAGAACAGTATTTCAT' ::::::::::::::::::::::::::::::::::::
1 4 GGAC	H H H	1. CGC(16 AGTATTT ::::::: AGTATTT
4AGG	GCCA	1 1 1 1	CAGT ::: -AGT
1440 .CGCC/	1510 GACT(1580 .ccag	1650 AGAA(::.
CATC	1 TGTG : T	GCAC	165 CTAAAGA : : : : : : CGAGAGG
) 1GAC	500 TTTATTT .:::: -ATATTT	GTT	CAGC
1430 TTCA:	1500 CTTT.	1570 GCCC	1640 TTGTTC::::::
4AGC	₩ CCC	rggr	CCGTI:::CTTTT
0 :AAC? ::	490 CCAGAA ::.:.: CCTGGA	CAG	30 ATTC(.:.
1420 IGACA :•: :	1490 GCCCA(. ::.	1560 AGACC	1630 GAAAT' : : GTA'
CTATA' :::.: CTAAA' 480	TTTG TTAG	ATTG.	SCAA ::· [CAG
1410 1420 CCTTCTCCCTATATGACAAC :::::::::::::::::::::::::::::::::	1480 1490 CAAACTATGCATTTGGCCCAGAA ::::: :::::: CAAACGC-TTAGATCCTGGA 500 510	1550 ATACCAACCCGATTG; •:: GTA	1620 Slit ACAGATCAAAAGCAA(::::. ::: ::: 325 ACAGTATAATCAG
1410 CTCTCC(::::	14 CTAT C	15 CAAC	16 ATCA : IA
CTTC' ::: -TTC' 470	CAAAC ::::: CAAAC	ATAC(.:: GTA5	ACAGA :::::
	slit C 325 C	slit A' 325 G'	lit A : 325 P
slit 325	S1:	S1:	32.3

Fig. 2M-6

1750 3GAACCA	1820 AGTTGCG	1890 ACGTAAA 	1960 GTAAATG
1740 CGCTGTGAA	1810 :ACACTGCAG: ::::	1880 TTCCTCAATT :::: TACCT	1950 AGCATCTGGT :.::: CTTCGG
1730 TGAAAAGTGI	1770 1780 1790 1810 1820 ATCAAAAAGCTCAACAAAATCCCGGAGCACATTCCCCAGTACACTGCAGAGTTGCG ::::: ::::::::::::::::::::::::::::::	1870 TTAAGAAACT	1940 MATTTGAAGGA:.
1720 rggcrrgccc .: AG	1790 CCCGGAGCAC ::: GGAA	1860 ACAGGAATCT .:: TGG	20 1930 ATATTGAGGAGGAGCAT .:.:::: .::. TTGTTGGTATGGTTGCT-
1710 TTGCGGATCTGG:::::::::	1780 CAAAAT	1850 IGTTGGAAGCC. :::::: TTGGGAG 650	1920 ACAGATATTG .::::
1700 TGGAGACTGCT	60 1770 TGCTCTAATCAAAAGC7 :.:: .::: TACTTAAATCTA	1840 ;AATTTACCGT(.:: TCC	1910 ACAATAAGATC.
1690 1700 1710 1720 1730 1740 1750 Slit CGATCAAAATTAAGTGGAGACTGCTTTGCGGATCTGGCTTGCCCTGAAAAGTGTCGCTGTGAAGGAACCA :::::::::::::::::::::::::::::	1760 Slit CAGTAGATTGCTCTA :::: .: 325TACTTAA	1830 1840 1850 1860 1870 1880 1890 1890 1890 1890 1890 1890 189	1900 1910 1920 1930 1940 1950 1960 ATAAACTTTAGCAACAATAAGATCACAGATATTGAGGAGGAGCATTTGAAGGAGCATCTGGTGTAAATG .::::::::::::::::::::::::::::::::::::
slit (Slit (Slit 325	Slit 325

Fig. 2M-7

2030 3CCTCAA :	2100 TTCTGTG	2170 CATTCTT	2240 AGTGGCT :
2020 GGATTGGAAA(2090 IAGGACTCAG	2160 rgatactctc	2230 GCTTGGTTGGGAG :::::::: GCTTGTTTGTAT-
2010 ATGTTCAAGO	2080 TGACAGTTTCA: :::::: TATCAGAATCAC	2150 CAGGGGCATT	2220 CTACCTGGCT' :::
2000 rgcagcataac	2060 2070 2080 AATAACCIGIGIGGGGAAIGACAGITICAT::::::::::::::::::::::::::::::::::	2140 ACAGTTGCAC	2210 ACTGTAACTG
1990 ITGGAAAATG:	2060 GAATAACCTG' ::::: -AATAACA'	2130 TCAAATTACT. 	2190 2230 2240 2240 2230 2230 2240
1980 ACGAGTAATCGT: ::::: GATTTATC	2050 AGAAGCAATC	2120 TGTATGATAA	0 2200 TAAACCTCTTGGCCAATCCTTT :::::::::::::::::::::::::::::
1970 1980 2000 2010 2030 2030 2030 2030 2030 203	2040 2050 2070 2080 2100 Slit AACTTTGAGAAGCAATCGAATAACCTGTGTGGGGAATGACAGTTTCATAGGACTCAGTTCTGTG ::: ::: :::::::::::::::::::::::::::	2110 2120 2140 2150 2170 CGTTTGCTTTCTTTGATAATTACTACAGTTGCACCAGGGGCATTTGATACTCTCCATTCTT :::::GCTTTC	218 TATCTACTC
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 2M-8

2300 2310 AAGAAATACCCATC ::::::GAAGTAC	2370 2380 crcccacrrrcrc:::	2440 2450 TTTGAAGGTCTTGCC ::::::::::::::::::::::::::::::	2510 2520 TGGTTCCCAAGGAA :::
2250 2260 2310 2310 2310 2390 2300 2310 2310 2310 2310 2310 2310 231	2330 2340 2350 2360 2370 2380 CAGGACTTCACTTGTGATGACGAAATGATGACAATAGTTGCTCCCCACTTTCTC :::::: AAAGTCTTAGAAGACTTTCTTTGTCTC 830	2400 2410 2420 2430 2440 2450 GTACTTGCTTGGATACGGTCGTCCGATGTAGCAACAAGGGTTTGAAGGTCTTGCC :: :::::::::::::::::::::::::::::::::	2470 2480 2510 2520 AGATGTCACAGAGTTGTATCTGGATGGAAACCAATTTACACTGGTTCCCAAGGAA ::::::::::::::::::::::::::::::
2260 2270 IGTCACGGGAAATCCTAGA1 :. :::: IAACAAAGTACC	2330 2340 CATTCAGGACTTCACTTGTGATG .:.:::: -TTAAAAGTCTT	2400 2410 STACTTGCTTGGATACAGT ::. :::: GCAATACAG- 860	2470 2480 AGATGTCACAGAGTTGTAT :
2250 2260 2270 GAGAAAGAGAATTGTCACGGGAAATCCT ::::::::::::::::::::::::::::::::	2320 CAGGATGTGGCCATT .:.	2390 GCTGTCCTACTGAAT:::::::::::::::::::::::::::::::::	2460 GAAAGGTATTCCAAG .: AA
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 2M-9

2530 2540 2550 2550 2570 2580 2590 21 2590 2510 2580 2590 2590 2590 2590 2590 2590 2590 259	2600 2610 2620 2630 2640 2650 2660 GCTTCAGCAACCAGCTCCTCACCTCTTAATTCTTAGTTACAACCGTCTGAGATGTATTCCTCCTCG :::::::::::::::::::::::::::::	2680 2720 2730 AAAGTCTCTTCGATTACTTTCTCTACATGGAAATGACATTTCTGTTGTGCCTGAA ::::::::::::::::::::::::::::::::::	2750 2760 2770 2780 2790 2800 CITICIGCATTATCACATCTAGCAATTGGAGCCCAACCCTCTTTACTGTGATTGTA .:.::::::::::::::::::::::::::::::::::
2530 2540 Slit CTCTCCAACTACAACATTTAAC :::::: 325TCCTGAAAAATTCAAGAA	2600 2610 Slit GCTTCAGCAACATGACCCAGCTC . :: : :::: 325 AATTAATAATCTTAA	2670 2680 Slit CACCTTTGATGGATTAAAGTCTC :::::::::::::::::::::::::::::::::	2740 2750 276 Slit GGTGCTTTCAATGATCTTTCTGCATTATC. : :: ::: :::: :::::::::::::::::::::::

Fig. 2M-10

DOTEMENT DINGER

2810 2850 2850 2870 Slit ACATGCAGTGATGTCGGAGTCGGAATATAAGGAGCCTGGAATTGCTCGTTGTGCTGGTCC :::: ::: ::: ::: ::::::::::::::::::	2980 2930 2940 Slit TGGAGAAATGGCAGATAAACTTTACTCACAACTCCCTCCAAAAATTTACCTGTCAAGGTCCTGTGGAT ::::::: 325 TTAATCTGTCAT	2950 2960 3010 3010 2990 3000 3010 GTCAATATTCTAGCTAAACCCCTGCCTATCAAATCCGTGTAAAATGATGGCACATGTAATAGTG ::::::::::::::::::::::::::::	3020 3030 3040 3050 3060 3070 3080 ATCCAGTTGACTTTTACCGATGCACCTGTCCATATGGTTTCAAGGGGCAGGACTGTGATGTCCCAATTCA .::::::::::::::::::::::::::::::::::::
Slit ACATG :::: 325 ACAT- 1090	Slit TGGAG : 325 T	Slit GTCAA : :: 325 -TTAA	Slit ATCCA .::: 325 GTCC

Fig. 2M-1

3090 3140 3150 3150 3150 3150 3150 3150 3150 315	3160 3170 3180 3200 3200 3220 TGGTGTATTTGTGATGGATTTGAAGGAGAAATTGTGAAGTTGATGA	3230 3240 3250 3260 3270 3280 3290 ACTGTGAAAATAATTCTACATGTCGATGGCATTAATAACTACACATGCCTTTGCCCACCTGAGTATAC ::::::::::::::::::::::::::::::::::	3300 3310 3320 3330 3340 3350 3360 AGGTGAGTTGTGTGAGCTTGTGTGCCCAGGACCTGAACCCCTGCCAGCACGATTCAAAG ::::::::::::::::::::::::::::::::::
Slit TGCCTGG: 325 T	Slit TGGTGT/ : 325 T	Slit ACTGTG; :::: 325 ACTG	Slit AGGTGA

Fig. 2M-12

O (1)	O () A	0 U U	O () ·· ()
3370 3380 3400 3410 3420 3430 TGCATCCTAACTCCAAATGTGACTGCACACCAGGGTACGTAGGTGAACACTGCGACATCG ::::::CATCCATGCGTGGCAGAGCATTACGTT	3440 3450 3460 3470 3480 3490 3500 ATTITGACGACTGCCAAGACAAGTGTAAAAACGGAGCCCACTGCACAGATGCAGTGAACGGCTATAC :::::::::::::::::::::::::::::::::	3520 3530 3540 3550 3560 3570 AGGTTACAGTGGTTCTGTGAGTTTTCTCCACCCATGGTCCTCCCTC	3590 3600 3610 3620 3630 3640 TTTGATTGTCAGAATGGAGCTCAGTGTATCGTCAGAATAAATGAGCCAATATGTC :::::::::::::::::::::::::::::::::::
3ACZ	35 3CTAT :: AT 1360	TCG.	SATAT(
i Idc(ACG(0 TCCCT::::TCACA	CCA.:
3420 ACAC	3490 GTGA	3560 TCCT(:::	3630 TGAGCC : C
3. GAA(CAG	3 ATGGT:::: ATATT:	3 AAT
GGT	ATG	CCAT.::AII.400	ATA
10 GTA ::. GTT	3480 :: :CACAG	3540 3550 3560 3571 TGAGTTTTCTCCACCCATGGTCCTCCCTCGTACC ::::::::::::::::::::::::::::::::	3620 TCAGA :: -CA
3410 TACGT ::::: TACGT	34 GCA :: TCA	3550 TCCAC:::::	36 GTC 1.
3410 AGGGTACGTA ::::: TTACGTT 1320	0 CCCACTGCAC : .:: :: -CATCTTCA-	540 GAGTTTTC: :: GTAAAATC: 1390	3610 3620 AGCTCAGTGTATCGTCAG :: :::::: -GCATAAAGTAACCA- 1440
00 CCA 1	0, 3,0,0,0 1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0	40 AGTT TAAA 1390	10 3TGT ::
3400 CACAC	3470 3GAGC	3540 3TGAG' : 13'	3610 CTCAGT : : CATAAA
ACTGC .:.: GCAGZ	AAC(HCH(AGC.
390 3400 TGTGACTGCACAC ::::::-:-:-:	0 AAA. .: TA 50	1 C T	1 GG
3390 ATGT :: GT(3450 3460 AAGACAACAAGTGTAA	3530 ACAGTGGCTTGTT:::::-::	3600 GAAT
CAA	AAG :	3. GTGGG:::	590 36 TGATTGTCAGA ::: ::: -GATGGCCTG-
ATT:	50 ACAAC :::: ACAAA	.: CI	90 GATTG :::: GATGG
3380 AGGG	3450 AGACAZ ::: TTACAZ	3520 GGTT : G	3590 TTGA' .:
3 AAA 	3 CAA :AT	35 3AAGG : : 1GAG-	
J I CO	OĐ L	10 GCCCCGA :: CCAG 1370	O GATAAT : ::: GCTAAT
3370 TGCATCCTAACT ::::: CATCCATGC- 300	3440 ;ACGAC :: AC	3510 GTGCATATGCCCCGA .:: :: :: :: ATGTATCCAG	3580 AGCCCCTGTGATAAT: :: ::: TACTGCGCTAAT 1420
3370 CATCCTAA ::::: CATCCATG	3, IGA(: • : IAA(3.5 *: ATA:	358(CCTGT(:: TGC(
GCA: -:: -CA:	34 ATTTTGAC::::: ATATTAAC 1330	3. GTGCATA' .:: :: ATGTAT-	 .:- AC−
slit 325	slit 325	Slit 325	Slit 325

1440 **Fig. 2M-13**

Fig. 2M-14

3990 CCCAAA	4060 TGCCAG	4130 CATCCG	4200 CCTGGC
3980 ATGGTGGGAAC .::::	4050 TGTAGGAGGCA	4120 TTCCACGGCTG :: TT	0 4190 CAAACAGGCATTTTG::::: -TTTTAATCATTTT- 1760
3970 TCTTTGTCCGTGG. :.::: -CAATGTC	4040 STCCACTCTA	4100 4110 TGGCAGAACGGAACCAGCTT : ::::::::::::::::::::::::::::::::::	4180 CGATGCAAA
3960 ;AGTCTCTTT(:.:: CAAT(4020 4030 CACTCTGAATTTTGACTC :::::::	4100 TGGGCAGAAC:::::: TTGACATTT1	4170 CAGAAGGTGC ::: GTG-
3950 CTTGGATCAG	4020 TCCACTCTGP::::	4090 .GCCAGGCCCC	4160 GCAGGACTTC
930 3940 ATTGTGGAACTACTTGC:::AATGATGCTGCTT	4010 GTCAAAGCAG :: GT	4080 GCATCTCTGC :::: GCTT	4150 ACAGTGAGCTG : ::: TTAGCTT
3930 3940 3950 3960 3970 3980 3990 Slit CTTCCACATTGTGGACTTTGGATCAGAGTCTCTCTTTGTCCGTGGATGGTGGGAACCCCAAA ::::: ::::::::::::::::::::::::	4000 4010 4020 4030 4040 4050 4060 Slit ATCATCACTACTTGTCAAAGCAGTCCACTCTGAATTTTGACTCTCCACTCTATGTAGGAGGCATGCCAG ::::::::::::::::::::::::::::::::::	4070 4080 4090 4110 4120 4130 Slit GGAAGATAACGTGGCATCTCTGCGCCAGGCCCCTGGGCAGAACCAGCTTCCACGGCTGCATCCG :::::::::::::::::::::::::::::::::::	4140 4150 4160 4170 4180 4190 4200 Slit GAACCTTTACATCAACAGTGAGGACTTCCAGAAGGTGCCGATGCAAACAGGCATTTTGCCTGGC ::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 2M-15

Fig. 2M-16

4540 4550 GACAGCTGTGATCG ::: : ::: GACTTCA-TAAACA 1940	4620 TTGCCAA ::: :: TTGA	4690 CCGCTGA : : ACTC	4760 agaaagt :.: aaa
4540 4550 3GGGACAGCTGTGATCG :::::::::-:-:	4600 4610 4 AGCAGCAGGCTATGCTGCTTGC ::::::::::::::::::::::::::::::::::::	4680 4 STGCTGTGGACCGC ::::::::::::::::::::::::::::::::	4750 4 GTGGACGAGGTTGAGAA ::::::::
4500 4510 4520 4530 4540 4550 TGGGGCAGCCCTACTGTGAATGCAGCAGTGGATACACGGGGGACAGCTGTGATCG ::::: -GGAGCAG	4600 461 AAGCAGCAGGGCTATG :::::::::GCA-CAGGTC-ATT 1970 198	4670 ?AGGAGGGCAC	4740 TCCTTTGTGG::::
4520 ATGCAGCAG1	4590 TATTACCAAA	4660 GTGGGTGTGC	4730 TGACGCCTCCTC .:. ::. TCAGTGCCA-
4510 CCTACTGTGA	4580 AAGGATAAGAGAT :::::: -TGAAAATGAG	4650 GAGTGCAGAG	4710 4720 AATACTCTTTCGAATGCAC ::::::::::::::::::::::::::::::::::
4500 CTGGGGCAGC ::::: GGAGCAG- 1930	4570 CGAGGGGAAAGG : :TGA 1960	4640 GTCCCGATTA	4710 AAATACTCTT : .::. :::. ATATTGTCTA
4490 Slit GCAGGCTTTCAGGTC :::::: 325 CCTGGCTT	4560 4570 4580 4590 4600 4610 4620 Slit AGAAATCTCTTGTCGAGGGAAAGGATAAGAGATTATTACCAAAAGCAGCAGGGCTATGCTGCTTGCCAA :: :: :: :: :: :: :: :: :: :: :: :: :	4630 4640 4650 4660 4670 4680 4690 Slit ACAACCAAGAAGGTGTCCCGATTAGAGTGCAGGGGTGTGTGCAGGGCCAGTGCTGTGGACCGCTGA :::::::::::::::::::::::::::::::::::	4700 4710 4720 4730 4740 4750 4760 Slit GGAGCAAGCGCGCAATTCGAATGCACTGACGCCTCCTTTGTGGACGAGGTTGAGAAAGT ::::::::::::::::::::::::
V.2	U 1	01	01

Fig. 2M-17

4830 AAAAGGTTG : . : ATATAATTA	4900 AAAATAC :::	
4820 4830 IGTCTTTGGAAAAGGTTG ::: :::.::.	4850 4860 4870 4880 4890 4900 TGTGGGACTAATGCTTCATAGTGGAAATATTTGAAATATTGTAAAATAC :: :::::::::::::::::::::::::::::::	
4810 CCGCCAGCTC	4870 4880 4890 CTTCATAGTGGAAATATTTGAAATATATTG : : : : : : : : : : : : : : : : :	4950 :: ::
4800 CTAAACACACTCC ::: :: AAACCTC	4870 :TTCATAGTGG :::.	4940 CTTTTTTCGCA : :: CGGCCGC-
4790 GTGTGTCCTAA :: AA	4860 TAATGAATGC :::::: TAATGAATTA 2100	4920 4930 4 TTATTATGAGAATAAAGACTTT :.:::::::: AAAAAAAAAAAAAAGGGCG
4780 CTGTACGAGGT ::: CTG	4850 CATGTGGGAC :: TGGAAATA 2090	4920 ITTTATTATG :
4770 4780 4810 4830 4830 830 831 4820 4830 811 GGTGAAGGTGTGTGTGTGTGTGTTTGGAAAGGTTG 1:::::::::::::::::::::::::::::::::	4840 Slit TATACTTCTTGACCA ::::::::::::::::::::::::::::::::::	4910 4920 4930 4940 4950 Slit AGAACAGACTTATTTTTTATTATGAGAATAAAGACTTTTTTTT

Fig. 2M-18

158 80 20 294 40 9 414 534 234 354 474 100 120 CTA GTA GAG 3CG CAG SCAGCTCTGGGGGGAGCTCGGAGCTCCCGATCACGGCTTCTTGGGGGTAGCTACGGCTGGGGTGTGTAGAACGGGGCCGGG GCTGGGGCTGGGTCCCCTAGTGGAGACCCAAGTGCGAGAGGAGAACTCTGCAGCTTCCTGCCTTTCTGGGTCAGTTCC Ы \triangleright 团 ď Ø ď TTATTCAAGTCTGCAGCCGGCTCCCAGGGAGATCTCGGTGGAACTTCAGAAACGCTGGGCAGTCTGCCTTTCAACC CTG GIG GGC CTA GAG Ы > r Ц Ø 臼 GAC CCC GAA GIG О Ø 闰 \gt \gt TCA GAC CAG CGC Ø Ŋ Ω 凶 ø Ы CTG ACC משש $\frac{1}{2}$ GGC ⋖ ט Z Ы Н \mathcal{O} GAG 390 TGG CGA GAG 团 വ് Ü 凶 口 GCC TAC TAC CTG GAA Ц × Ц K 回 \succ GAG GAG TIC GGC GCT Ü ∢ Ы 口 団 ഥ TGC GCG CCG CCT GGT \mathcal{O} \mathcal{O} Ø > Д Д CCC GAC AGC 9999 GCG Ø Д Д വ വ r EGG CCC CTG GTG GTG 口 \triangleright \gt Ü Д ⋈ TGC AAA CGG ATG CAT U × ഷ 田 \Box Σ GAG GCA CGGG GCT CTT Ø ద Ц ᆸ Ø 江 GAC GCC GGC TGG GGG ᠐ Д Ø Ω Ü ⋈ GGA ACA CAG GCA TAC Ø ď Z ⊱ Ü <u>-</u> CIG GGC GIG AAA TTT Ц r \triangleright \bowtie ᅜ α CC CIG CC TCA CAA Ы \circ Ŋ Д ß Ŋ CAC GTG GGG GCA ď \triangleright Ç Д 耳 CCC GIG GTG CTG CTG Ц ᆸ \gt Д > ATG CTG ACT CAA CTA Ø Н Ц ⊟ Д Σ

Fig. 3A

594

GCG

CAG

GIG

GCA

AAC

CGC

CTG

CIC

GTG

TCA

CCC

GAC

CTG

CCC

AAC

CGC

CCA

CCC

CCG

CCG

140 654 160 714 180 774 200 834 220 894 240 954 260 1014 R E S AGC R CGC P L CAC TAC 田 \succ P L CTA S I ATC IGG Q CAG S TCA ⋈ A GCC H CAC A GCA G GGG CAC P L 耳 P PCCA K AAG TACC N AAT AAT PCCT z AGC S AGC F M ATG I ATC GGT CAA P Ø G G G PCCT G GGC S TCC S AGC AGG GAC Q CAG 吆 \Box A GCC E GAG R Q CAA GGG N AAT R GAA ŋ 口 L S AGC GAC A GCT S AGC L E GAA П S TCC S TCA T ACA Q CAG GGC P S AGT \mathcal{Q} C TGC TACG T ACC P V GTG L AGG L ద S S AGC L TACA $\frac{L}{TTG}$ L GTG C \gt K AAG A GCC GGC H V GTC P GGC TCT Ŋ CGG A GCA K AAA F GCC L PCT CCT Д ď V GTC C TGC V 3TG L E GAG GAG M ATG H CAT ſΉ T ACC **3AG** L GAG TCA ICC A GCT GCT ഥ Ø Ø Ω L TACG TACC V GTG V GTG GGA L Ŋ D GAC EGAG R CGA GGC V GTC VGTG TIC EGAA Q CAG \overline{W} A 3CC R AGA g GGC L ICC C IGT ß 3AG G GGC R G GGC TACC GCT T ACT GTG Ø \gt E V GTG L CAC I ATT L S 江

Fig. 3B

380 1374 340 1254 360 1314 320 1194 400 1434 420 1494 Q CAG R AGG A GCC P E GAG GGG L ITG E GAG R CGG R AGA N AAT S TCT LCTC A GCC ₽ K AAG E D GAC I ATC L S AGC A GCA A GCC R CGC S TCC G GGG S AGT GGG V GTC E GAA \mathcal{Q} Q CAG I ATC N AAC M ATG R GTA DGAT H CAT \gt GTG E GAG GTG C P V GTG H CAT S AGT \gt E GAG TAC R AGG V GTC D GAC GGT S TCT R CGA \succ T ACC E GAG C TGC Y TAC VGTG R CGA V GTA LCTT P S AGC I ATC V GTG S TCC L 3GG V GTT Ö M ATG TACC Q CAG S AGT GGC V GTG D GAT S AGT N AAC S AGC V GTG VGTG L L P S AGC D GAC R AGG E GAG S TCG V GTG L H CAC TACT K AAG V GTC A GCC GTG E GAG P E CCT \gt Д L CTC V GTG E GAG D GAC Q CAG S TCA G GGG T ACT T ACC V GTG Y TAT T ACG S AGT GAT S TCT GIG \gt Ω D GAT VGTG K AAA H CAC r CTG L D GAT L Q CAG PCCT CGG R AGG D GAC L H CAT CCA 엄 Д V GTG TACC S TCC H CAC S TCA P L ACA H G GGC M ATG CAT IGG TTT S TCC Q CAG C TGC 工 ഥ E GAG L CIG K AAG F Q CAG G GGC F N AAC

Fig. 3(

460	1614	480	1674
ы	CTG		CAG
闰	GAA	N Q	AAA
₽	ACT	Н	ATC
O H	CAG	ט	GGC
H	ACA	团	GAA
闰	GAA	Д	GAT
	ATA		CAG
团	GAG	О	GAT
ద	AGG	田	GAA
V R	GTG	闰	GAG
⊢	ACG	闰	GAG
⊣	ACC	闰	GAG
Н	CIG	A	Ö
	ACG		CGG
S Y S	ICC	ΰ	GGG
×	TAC	Ø	$_{ m TCT}$
യ	AGT	Ф	GGC
ద	CGC		TCT CCA
口口	GGC	യ	
团	GAG	П	CTG

200	1734	511	1767
ϋ	GGC		
T G N G	AAT		
ъ	GGC		
⊢	ACG		
Д	CCC		
R A K P	AAG		
¥	BCC		
ద	CGG		
Ы	CTA		
⊣	ACC	*	TGA
U	GGG	* ^	GIC
N G	AAT	口	CTG
闰	GAG	Ħ	CAC
Ø	CAG	ტ	GGA
>	GTT	ద	CGG
ᄄ	TIT	ט	GGG
H	CAT	Z	AAT
Z	AAC	Н	ATC
Σ	GCC ATG	×	TAC
Ą	CCC	Н	ATC

CAC

GGA

CCCC

999

AAT

ATC

TAC

ATC

1925 2478 1846 2004 2320 2399 2557 2241 2083 2162 CTGACTGTGTGTGTGTGGAGGGGTGACTGTCCGTGGAGGGGTGACTGTGTCCGTGGTGTGTTATTATGCTGTCATATCAG GGAGGAGAGAGAGACTGTGGCTCAGACCCAGGTGTGCGGGCATAGCTGGAGCTGGAATCTGCCTCCGGTGTGAGG GTTACAGAAGCCCTCTGCCCTCTGGTGGCCTCTGGGCCTGCTGCATGTACATATTTTCTGTAAATATATACATGCGCCGGG TTTTATTTATTTTTTTTTTTTTTTTTTTTTAGAGATGGAGTCTCACTATGTTGCTCAGGCTGGCCTTGAACTCCTGGGC CCCAGGCCTGCCTTCCCTAGGCCTGGCTCCTTCTGTTGACATGGGAGATTTTAGCTCATCTTGGGGGCCTCCTTA AGTCAAGTGAACTGTGGTGTATGTGCCACGGGATTTTGAGTGGTTGCGTGGGCAACACTGTCAGGGTTTGGCCTGTGTGT CATGTGGCTGTGTGTGACCTCTGCCTGAAAAAGCAGGTATTTTCTCAGACCCCAGAGCAGTATTAATGATGCAGAGGTTT GAACCTGTCTCCTACCACTTCGGAGCCATGGGGGCAAGTGTGAAGCAGCCAGTCCCTGGGTCAGCCAGAGGCTTGAACT

Fig. 3E

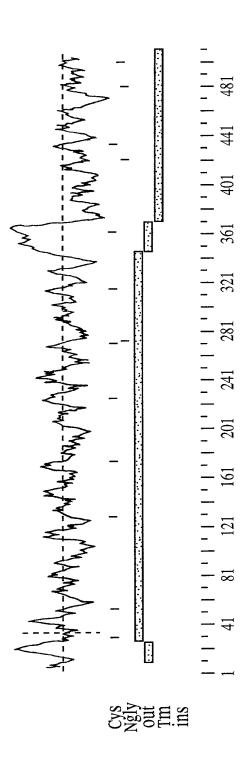


FIG. 3F

39 59 178 79 99 119 358 139 418 159 TCC GCT GCT D GAT ACC Ø ď ď s TCT L CTA H S TCA GTG L GGA r CTG L CTG GAT ტ D GAC \gt Ω T ACC GTG F TTC GAA CGG \triangleright P CCA AGG ഥ GTG ద 卍 > IGI S TCC R AGA T ACA P ט S TCA Q CAG ø GTG 3GC TGG Н > TTT S TCC AAG Ü ⋈ ഥ × A GCT CIG CAC I ATT N AAC g GGC 出 口 TTC GGG ഥ Ü S CCA L H Y TAC Д TTG GAG ICT 니 口 Ø R GGC Q CAG I ATC W TGG S TCA TACT AAT GAC О z S GGG H CAC L CTG P D GAC S AGC Ö GAA 闰 H CAC N AAT T ACC N AAT P G G G G V GTC CAG Q AAG × ATG I ATC Q CAA P D GAT H CAT Σ P CCC F TTC S AGC R AGG D GAC Q CAG V GTG C TGC GAC Д S TCC R CGC Q CAA E GAA G G G R CGA GTC A GCA > R CGT S AGC D GAC LCTT E GAA V GTA Y TAC L S AGC CCT Q CAG G G G S AGT . GGG I ATC VGTT Д JCC GIG L CTC R AGG L S AGT g GGC D GAT TACG TTG L GTG C P S AGC V GTG > TACA CAC GGC S TCT K AAG L H T ACT G GGC TIC PCCT A GCC LCTC P GAG GIC > C AAA 口 GAG H CAT E GAG M ATG GGG T ACT Q 口

Fig. 3G

179 538	199 598	219 658	239	259	279	8 7 8 8 8 8
V	K	H	T	E	ტ	V
GTG	AAA	CAC	ACG	GAG	ტ	GTC
L	Q	H	T	E	N	L
	CAG	CAT	ACC	GAG	AAT	CTG (
L	T ACC	S TCC	L	A GCC	E GAG	H CAC (
C	M	H	T	R	Q	GGA (
TGC	ATG	CAT	ACG	CGG	CAG	
F	Q CAG	L	S TCC	ტ ტტ	V GTT	R CGG
L TTG	Q CAG	R AGG	YTAC	S	H H H H	9
CIC	A GCC	R CGG	S AGT	3 3 3 3	H CAT	N AAT
A	K	I	R	P	N	I
GCA	AAG	ATC	CGC	CCA	AAC	ATC
A GCC	R CGC	S	g GGC	S	M ATG	Y TAC
I	R	N	E	L	A	I
ATC	CGG	AAC	GAG		GCC	ATC
V GTG	H	E	P	CTG	Q CAG	0 00 00 00
G	Y	R	E	E	K	N
GGT	TAC	AGG	GAG	GAA	AAA	AAT
V	R	T	E	T	I	
GTG	CGA	ACC	GAA	ACT	ATC	GGC
V	S	L	S	Q	G	T
GTG	TCC	CTG	AGT	CAG	GGC	ACG
V	M	T	Q	T	E	P
GTG	ATG	ACC	CAG	ACA	GAA	
V	CIC	L	S	E	D	K
GTG		CTG	AGC	GAA	GAT	AAG
S	V	E	R	I	Q	A
TCG	GTG	GAG	AGG	ATA	CAG	GCC
A GCC	V GTG	E	P	E GAG	D GAT	R CGG
S	V	E	D	R	E	L
	GTG	GAG	GAC	AGG	GAA	CTA
V GTG	V GTG	Y TAT	TACG	V GTG	EGAG	TACC

* TGA

300

IOPERSI OIIGO

CCCAGGCCTGCCTCCCTTCCCTAGGCCTGGCTCCTTCTGTTGACATGGGAGATTTTAGCTCATCTTGGGGGGCCTCTTA	980
AACACCCCCATTTCTTGCGGAAGATGCTCCCCATCCCACTGACTG	1059
GAGGGCTCCACCAATTGAGTCTCTCCCACCATGCATGCAGGTCACTGTGTGTG	1 2 2
CTGACTGTGTGTGTGTGGAGGGGTGACTGTCCGTGGAGGGGTGACTGTCCGTGGTGTGTGT	1217
AGTCAAGTGAACTGTGGTGTATGTGCCACGGGATTTGAGTGGTTGCGTGGGCAACACTGTCAGGGTTTGGCGTGTGTGT	1296
CATGTGGCTGTGTGTGACCTCTGCCTGAAAAGCAGGTATTTTCTCAGACCCCAGAGCAGTATTAATGATGCAGAGGTT	1375
	1454
GAAUCTIGITUTICCTACCACTTURGGAGCCATGGGGGGGGAAGTGTGAAGCAGCCAGTCCCTGGGTCAGCCAGAGGTTGAACT	1533
	1612
	1691
	1770
	1849
CGAAGAGAAAAAAAAATTAAAGAAAGCCTTTAGATTTTATCCAATGTTTACTACTGGGATTGCTTAAAGTGAGGCCCCT	1928
	2086
	2165
_	24
	2323
	2402
TGTAAATATGTGCATATTTGTACATAAAATGATATTCTGTTTTTAAATAA	2481
ACAGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2510

Fig. 3]

EAWLLLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWARV 20 30 40 50 60 70		HSKYGLHVSPAYEGRVEQPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQAR 90 100 110 120	10 20 KGTTSSRSFKHSRSAAVTSEFHL	::::::::::::::::::::::::::::::::::::::	30 40 50 90 90 VPSRSMNGQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY ::::::::::::::::::::::::::::::::::
MPLSLGAEMWGPEAWLI 10		DAGEGAQELALLHSKYG 80		LRLRVLVPPLPSLNPG 150	30 40 ALT VPSRSMNGQPLTCVVSH :::::::::::::::::::::::::::::::::::
T364	ALT	T364	ALT	T364	ALT 1

Fig. 3.

160 KQVDLVSAS ::::::::); ; ?PEESVGLR	MNHFVQEN ::::::: MNHFVQEN	
150 ADPQEDSGI :::::: DPQEDSGI 340	220 SHHTDPRSÇ :::::::: SHHTDPRSÇ 410	270 DQDEGIKQA :::::::: DQDEGIKQA 480	
140 DSQVTVDVI :::::::: DSQVTVDVL 330	210 RENSIRRLH ::::::: RENSIRRLH 400	260 3SGRAEEEE :::::::: 3SGRAEEEE 470	
130 CHVSNEFSSR:::::::CHVSNEFSSR:320	200 QKYEEELTLT] :::::::: QKYEEELTLT] 390	250 STQTELLSP(::::::::: STQTELLSP(460	
EHSGIYV ::::::: EHSGIYV 310	RKAQQMT ::::::: RKAQQMT 380	230 240 250 260 270 ALTSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQEN ::::::::::::::::::::::::::::::::::::	
O 120 GDTLGFPPLTT ::::::::::::::::::::::::::::::::::	190 VVLMSRYHR: ::::::::: VVLMSRYHR: 370	230 EEPEGRSYS :::::::::::::::::::::::::::::::::::	GHLV :::: GHLV 510
110 PSGVRVDGE :::::::: PSGVRVDGE	180 ALLFCLLVVV ::::::::: ALLFCLLVVV 360	S : :KDNSSCSVMS	290 'GNGIYINGRG ::::::::::
100 NWTRLDGPLPSGVRVD :::::::::::::::::::::::::::::::::::	170 180 VVVVGVIAALLFCLLV ::::::::::: VVVVGVIAALLFCLLV 0 360	EGHPDSLKI	0 TLRAKPTG ::::::: TLRAKPTG 5
ALT N::	ALT V : T364 V 350	ALT - T364 A	280 ALT GT] :: T364 GT]

Fig. 3K

CTCTAGCAGGAGGTCTCTTGGGCAAGTCTTTAGGGAGGGGAGGTGTGTTGTCCCTGAG CTCTAGCTTCTTTAAATGAGGTCTCTCTGGGCAACATCTTTAGGGAGGG	52	134	<u>ر</u>	7 0
CTCTAGCAGGGGGAAGTCTCTTAGTCCTATGAGAGTGTGTAGCAGTTTGTCCCT CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCAACATCTTTAGGGAGGAGGGTACAAAAGGTTCCTGGACCTT M M Q E Q Q P Q S T E K R G AACACAGGGAGCCTGCATA ATG ATG CAA GAG CAG CAA CCT CAA AGT ACA GAG AAA AGA GAG	rga G	CTC	M	T.
CTCTAGGAGGTGTGTAGCAAGTTTGG CTCTAGCTTTTAAATGAAGGTGTGTAGCAGTTTTGG CTCTAGCTTCTTTAAATGAAGGTGTCTCTGGGCAACATCTTTAGGGAGAGGGTACAAAAGGTTCCTGG M M Q E Q Q P Q S T E K R AACACAGGGAGCCTGCATA ATG ATG CAA GAG CAG CAA CCT CAA AGT ACA GAG AAA AGA	[מממ]	VCCT1	Ü	
CTCTAGGAGGTGTGTAGGCAAGTCTTTAGGAGAGTGTGTAGCAGG CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCAACATCTTTAGGAGAGAGGTACAAAAGGTTCC M M Q E Q Q P Q S T E K AACACAGGAGCCTGCATA ATG ATG CAA GAG CAG CAA CCT CAA AGT ACA GAG AAA	[TTG]	TRGGZ	ద	AGA
CTCTAGGAGGTGTGTGTACCTTAGGAGGTGTGTGTACCTATGAGAGTGTGTACCTACC	3CAG.	3TTC		AAA
CTCTAGGAGGICTCTTTAATGAGGGGCAAGGICTCTTTAGGGAGGGGGGGGGG	IGTA(AAAGC	ĿΊ	GAG
CTCTAGGAGGTCTTTAAATGAAGGTCTTTGGGCAAGGTCTTTAGGGAGAGGG CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCAACATCTTTAGGGAGAGGGG M M Q E Q Q P Q S AACACAGGGAGCCTGCATA ATG ATG CAA GAG CAG CAA CCT CAA AGT	\GTG.	raca <i>i</i>	H	ACA
CTCTAGGAGGTCTCTTTAAATGAAGCTCGAGTCTCTGGGCAACGTCTTTAGGGAGACACATCTTTAGGGAGACACATCTTTAGGGAGACACACATCTTTAGGGAGACACACATCTTTAGGGAGACACACATCTTTAGGGAGAGACACACAC	rgag2	3AGG]	വ	AGT
CTCTAGCAAGTCTCTTTAAATGAAGCTGAGTCTCTGGGCAACATCTTTAGGC M M Q E Q Q P AACACAGGAGCCTGCATA ATG ATG CAA GAG CAG CAA CCT	CTA	3AGA(Ø	CAA
CTCTAGGAGGTCTCTT CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCAACATCTTT M M Q E Q Q AACACAGGAGCCTGCATA ATG ATG CAA GAG CAA	ragT(ragg(Д	CCI
CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCAACACACAC	CTCT.	[CTT]	Ø	CAA
CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCZ CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCZZ M M Q E AACACAGGGAGCCTGCATA ATG ATG CAA GAG	AAG'I'(AACA	Ø	CAG
CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTC M M Q AACACAGGGAGCCTGCATA ATG ATG CAA	1.T.G.G.	70995	闰	GAG
CTCTAGCTTCTTTAAATGAAGCTGAGT(4A'I'G	CICI	Ø	CAA
CTCTAGCTTCTTTAAATGAAGCTC M AACACAGGGAGCCTGCATA ATG		jAG'I'(Σ	ATG
CTCTAGCTTCTTTAAATGA; AACACAGGGAGCCTGCATA	<u>i</u> 7	AGC'I'(Σ	AIG
	F T E E E E E E E E E E E E E E E E E E	CICIAGCIICIII AAAIGA		AACACAGGGAGCCTGCATA

15 198	35 258	55 318	75 378	95 438	115 498	
™ TGG	F	S	A GCC	S AGT	V GTT	
GGC	C TGC	L	P	S TCC	L TTG	
r AGA	A GCT	R AGG	V GTG	I ATT	H CAT	
A AAA	S AGT	K AAA	K AAG	F TTC	A GCA	
GAG	L	G GGC	T ACA	Y TAC	G GGA	
ACA	L	T ACT	GGG	C TGC	M ATG	
AGT	A GCA	E GAA	E GAA	S AGT	E GAG	
CAA	I ATT	G	S AGT	S TCC	V GTT	
CCT	S TCC	Y TAT	F TTC	GGT	C TGT	
CAA	I ATT	T ACA	\mathcal{C}	F TTT	N AAC	
CAG	ტ ტტ	TTT TTT	T ACC	S TCA	Q CAG	
GAG	A GCT	H CAT	CIC	K AAG	E	
CAA	V GTG	Y TAC	S AGT	W TGG	S AGT	
ATG	S TCT	TACT	S TCA	S TCT	K AAG	
ATG	W TGG	V GTA	H CAT	A GCT	S TCT	
CATA	L	V GTA	Y TAT	PCCA	W TGG	
CCTG	R AGA	C TGT	S TCA	C TGC	V GTT	
3GAG(L	S AGC	H CAC	C TGT	K AAG	
AACACAGGGAGCCTGCATA	S TCC	V GTG	L CTA	G GGA	E	
AAC;	Γ	I ATT	E	\overline{W}	E GAA	

Q CAG

Q CAG

F I V TTC ATT GTC (

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E

E GAA

F N T TTC AAC ACA (

V GTG

TGATTCAATCAAGTTTGGCAAGCAGGGTGTTCGATACTGCTATATCCTGTATTCTTGGTTTTATTTTATTTTCTGAG AAGCATTTCTTGTTACCCAAATCTAACCTATTCCTGAAAATATGATGGTTAGCAAAGTTTGAGATAACTAGAGCCTGTA TACCAAAATGGTCATTAATCTGTATCCACAAAGGATTTCTGCATTACATACTTTAAAACAAATTACCTAATTATTAGT

1652

155	618	175	, о С	738	210	783	862	941	1020	1099	1178	1257	1336
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×	AAG	が 日 で	} ;	TGT			CTAT	TGTI	TTCZ	TTGI	GTCZ	CATG	TATA
Q	ATT GAT	A ک م	; ; ;	F GAT GTT ATC			ATTACTGACGTAATTTTTCCCTGACGTCTTTAAAATTGAACCCTATCAT	TACC	CCATTAATGATAGAATGCACCCTTCCTCTTTTGTTCCATTCTTTCACTT	CATTACACAAATATTTATTGTTTCAGAGACTGTACTATTTTGTTTG	TTATGACTTTCCTTCCATATACCATAAGAAATCTTTTTGGTCAAGA	CCTGACAAGAGTTGAAAGACATGTTTTCTAGATGGCTCACTCA	CTGGAAATAAATTTTATTCTGCAGTTAGGGATTTTGGCATTTTATATGT
Н	ATT	H S	; } }	GTT			ATTG	AAAGA	TCCZ	TAT	TCTI	CTCA	GCAT
M	TGG	H CAT	; -	GAT			TAAZ	TGGA	TTGI	GTAC	GAAA	ATG	TTTG
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M	TGG	P CCC 2) }	: TGG	ц	CTA	GACG	CACE	TCCI	CAGA	ACCA	TTTT	GTTA
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ŋ	$^{ m GGL}$	H	E-	ACA	Z	AAT	BACGI	TTA	TGA	CAAZ	TTT(AGAG	TAAZ
Ø	CAA	W TGG		CCI	Σ	ATG	PACTO	AATC	TTAZ	TACE	TGAC	'GACZ	GAAZ
Д	CCA	F	×	AAA	闰	GAG	BAATT	ACATZ	LTCCZ	[TCA]	ATTZ		ACCIO
Д	GAC	R AGA		TGG	บ	LGT	AGAAC	TACZ	CTTJ	ACACT	GAA7	GAAC	'GTA
യ	TCA	GTC	<u>[</u> ±,	TTC	Н	ATA	BAAG	BAATI	rrcci	TLC	TLL	ATCI	rtaat
ᄓ	CTT	N AAT	\triangleright	GTC	W	TCA	BAAAC	CCT	rcgī	TLT.	FTAT(AAT	3CTA1
ტ	GGG	K AAA	H	ATA	Z	AAT	\TTG([TCT]	CTTC	LTTT(3GCA(ACTA(FTTG(
Н	CTG	E	Ø	TCA	껁	AGG	CTTA	[AAT]	ZAAT(\TTT\	TAA(rgg <i>A</i> 2	rggT(
Y F L G L S D P	m LLL	P Y E K N V R F W CCT TAT GAG AAA AAT GTC AGA TTT TGG	Ø	TGT GCT TCA ATA GTC TTC TGG AAA	ద	ACT AGA AGG AAT TCA ATA TGT GAG ATG	GTAGAAGCTTAATTGGAAAGAAGAGA	GAAATGATAATTTCTTCCTGAATTTACACATAATCCTTATGTTATAGAGGTTCACAGAAATGGAAAGATACCTGTTTCC	CTTTAATCAATCTTCTCGTTTTCCTTTT	GTTATTCATTTTTTTCTTTCTTCACACTT	AAGATTTATAAGGCAGTATCTTTTGAAAA	TGGTAGTTGGAACTACAATCATCTGAAGG	GGCAACTTGGTGTTGGCTATTAATGTAAC
×	TAT	CCT	ט	IGI	H	ACT	GTAC	GAA?	CTT.	GTT?	AAG?	TGG	GGC7

Fig. 41

2126 2205 2442 2363 2600 2679 2758 2521 2916 2837 TGGCAGTAGGAGCCTATAAAGGGATAAGCAATTGGGAAAGGATTGGGAAGTTGGTAGTACTGAACATCTTCTCACCTGG GGCACAACAATTTTTAAATTTAATTTTAGCAAATATTTTGGATATTAAAGCTTCTTATAGAAAGAGATACCTGTATATTTTA TTCTTTAAATTTTAGTAATGCCTTTGGCTTTTAATTTTTCTCCTGATATAAAATAGATACAGTAACTTTCATTATGTTAG ACTCATGAGCAACTTGAATAGTTGTAACTGTGATGCATATGTAGATTCTAACACACATTTTTCCCCCTTGAATAGAAATTT TGCTGTAAAATTTTTTTTTCCATCTTCTATTTTTGACCATTTTTATTCCACATGTGCTCTTAATAAGTAGCATATAGTT AAATTTTAAAAAATCCAATATGGCAATCACCTTTTAGGTTAAAAATTTTAATCCATTTTACATTTGTGACAATTCGACATA ACAACTTTTTATTAGAAAGTTATACATAACACAGCATCAACTATTTTCAAGAACCCAATAAGCAACAAAAAACCAGACTA ACAAAATGTGTAACAAGAAACTAATGACCTTTCTAAAATCAAACATTCAATTATCTACAATGTCTATTTTACAAACAGGG AAAACTCCATGGTTTACAGGCATGTCATATTGAAAATAAAGCTGCAATAGCTTTTTATACAATTATGCTCTCTCAAGAAA ATGAATCATTAAGACAGTAATTAGGAGTTCACAAATTTAAAACATTTCACGTAATTTTAAATTTATTGTCTTCAATAATT TTAAATTATTGAAGTCTGAGTTTTCAAAAGTGATTTTTTCCCACAAAGGTGCCAACACTTAAGCTAGAGCTTTCAGTGTT AACTTTGCCCTAAAAGTTAAGACATATTCTGAGAATCATAATAGTCACATGATTTCTGATGCTATCTGCTCTGTTAATA ACAAAGATTTCACACATGAATACCTATGTAACAAATCTCCATGTTCTACACATATACCCCAGAACTTAAAGTATAA

Fig. 4C

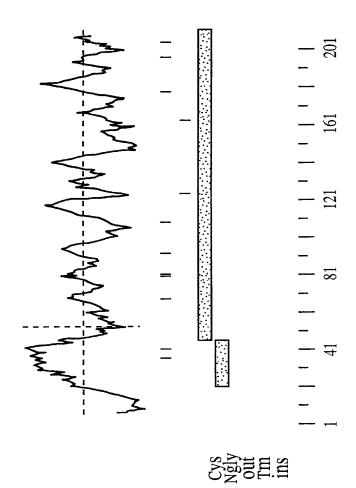


FIG. 4L

158 SAACTCTGGCCTCTTTGACAGAAGCCAGGTCCCTGAGTCGTATTTTGGAGACAGATGCAAGAAACCCTGACCTTCTGA

16 221 36 56 9 / 96 281 341 401 461 521 L CTG AGC IGG GIG CAC AAG Y TAC S Н \succeq \gt 3 T ACC GCG CTT ATG S TCT ACC GIG > ø \boxtimes H IGG I ATT GAA Γ LCTT AAA TCT ≥ × 闰 Ŋ C TGC F IAT GAA ATT CAT TCA \succ [±] Н Н വ GIC L CTA CTGT S TCA CIC GAG A GCT П \triangleright 더 GGA ACC AGA GIG TAC G G G AAT ᠐ \succ \gt ₽ ĸ z AAG M ATG S AGT AGA IGC M ATG CTG U \bowtie Н α GGG TTGQ CAG AGT ACT AGC CAG ß Ø \mathcal{O} \vdash ⊢ ഗ Q CAA L CTC CCC GGG TCC CAG V GTT Д ტ ß Ö TCC CAG ACC TTA GGC $_{\rm TGT}^{\rm C}$ GAA \vdash Ø \Box H S 囗 AIG ATC Q CAA GAC AGT TTTN AAC \Box \sum Ŋ ᄺ Н AGA S TCC ATG $_{
m LLC}$ Q CAG TIC TCA \simeq \boxtimes ᄺ ፲ Ŋ GAA I ATT ATT IGC K AAG E GAG AAT ر ک Z ഥ Н CAG V GTG FTTT ACC TGG CAG S AGT ⊣ \boxtimes Õ Ø GIG CIC GAG A GCT Q CAA H CAC T ACC П 冝 ATG CCT IAC AGT N AAT S AGC GCG \succ S ø X ACATACACCTCAACA T ACT P CCA W TGG E GAA TCA ICC S S IGG GIG C F TACT H CAT \gt S L GTG TAC C TGC N AAC N AAT \gt \succ I ATC IGT E GAG AGA T ACA GGA U Ü

Fig. 4E

G G F K	F L G L TTC CTG GGT CTT S V K M	S H CG S	S D P TCG GAT CCC		K AAG G	V GTA T	M ATG P	A GCA M	N AAT N	G G P	N AAT I	AAG GTA ATG GCA AAT GGC AAT GGA TCG ATG ATA CTC CTT G T P M N P I F Q K S G V	7 CG	M ATG K	I ATA S	CIC	CTT V	156 641 176
TCA GTC AAA ATG		TCA	TCA GGT TCT	TCT	GGC ACC CCC ATG AAC CCA ATC	ACC	CCC	ATG	AAC	CCA	ATC	TTC CAG	CAG	AAG	AGC	AGC GGT	GTG	70
E Ç	-	ب ب ر	(E C	, , ,	Ę Ę	E	E C E	£ Ç E	[[, , , , , , , , , , , , , , , , , , ,	ξ ξ	ξ ξ Ε	E	ς ζ ξ	; E *	۶ ۱ ۲	710
).T.T.)		GARA	75.E.E	אבר ה	S G G A.A.	T.GA.I	֡֝֟֝֟֝֟֝֟֝֟֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֟֓֓֓֟֓֓֓֟֓֓֓֓֓		JI GA	I AGT	-AAAC	ACAAT	LTCAA	VI.A.I.	JIGA	AATG	AANA	ν α
AGATTACCTATGAATGCCTGTTATTCTTAATA	ďη	CCIC	FTTA1	TCTI	'AATA													821

Fig. 4F

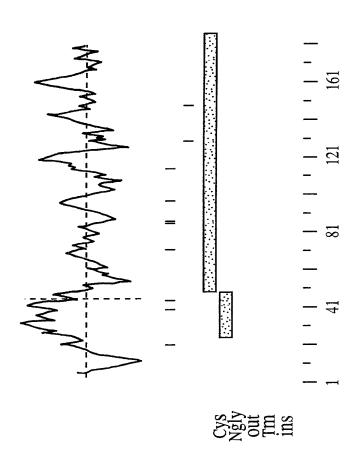


FIG. 46

70 FSEG: FSEG:	SYFL SYFL	200 ETRRNSICEMNKIY : :: -TPMNPIFQKSGVF 170
SLIC	VESE VESE	CCEMI : •• [FQK:
09 09 09	130 2011 2011 130	200 FRRNSIC: :: FPMNPIF
ELHS FLHS ELHT	N FIV	CETR TF
KRLS .:: RRLY O	O EAEQ EAEQ	NDV I
50 3ETGKI DQPSRI 50	120 /FNTE/ : .: :: : /INTE/ 120	190 3wGwni : :
SLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEG ::::::::::::::::::::::::::::::::::::	110 120 130 SEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFS :::::::::::::::::::::::::::::::::::	140 150 160 170 180 190 200 human GLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIY ::::::::::::::::::::::::::::::::::::
VTYF :::. VTYÇ 40	110 :VEMG? : • : : : : : : : : : : : : : : : : : :	180 SIVEW:
40 VSCV · · · · · · · · · · · ASCV	DNCV :::: QNCV	2 QCAS : :ILLS
ACEI TCEI	S KS S TS E	HSAE NGSM 0
30 ALLS: ::: LLLS'	SSCYFISSEEKVWSK:::::::::::::::::::::::::::::::::::	170 GEPNH:
20 SLRLWSVAGISIA .:::::::: TLRLWSAAVISML 20	LSSE.	TWHT.
WSVAC:::WSAAV	90 SCYE:: SCYL	SO KNVRI
20 ILRLW ::::	F G S S S S S S S S S S S S S S S S S S	160 'PYEKN'
GWLS 	SWKS .:: HWKS	I DKT
10 STEKR GKGVC	80 WGCCPAS' :::::. WGCCPNH'	150 NWQW :
10 2PQST. 2SQGK	WG :: XMWG	2GNN · KVMA
1 MQEQQPQS :.::.:.: MVQERQSQG	IKVPA- :.: IMVSER	CESDE ESDE ESDE O
n e M	.n TKV :.: e TMV	140 .n GLS ::: le GLS
10 30 40 50 60 70 human MMQEQQPQSTEKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEG ::::::::::::::::::::::::::::::::::::	human TKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL::::::::::::::::::::::::::::::::::	140 150 human GLSDPQGNNNWQ :::::: murine GLSDPKVMAN
Ħ	æ	Ħ

human L

murine Q

₹ig. 4H

20	90 100 110 120 130 140 CACTCCTCAGTGCTTCATTGTGAGCTGTGTAGTAACTTACCATTTTACATA ::::::::::::::::::::	160 170 180 200 210 AAGGCTGTCTGAACTACACTCATTCAAGTCTCACCTGCTTCAGTGAAGGG :::.:::::::::::::::::::::::::::::	230 240 250 260 270TGGGGATGTTGCCCCAGCTTCTTGGAAGTCATTTGGTTCCAGTTGCTACT ::::::::::::::::::::::::::::::::::
10 20 human ATGATGCAAGAGCAGCAACCT :::::::::::::::::::::::::::::::::	80 CTGGGATTTCCATTGCACTG ::: :::::::::::::::::::::::::::::::::	150 160 170 180 190 200 210 TGGTGAAACTGGCAAAAGGCTGTCTGAACTACACTCATATCATTCAAGTCTCACCTGCTTCAGTGAAGGG : : : : : : : : : : : : : : : : : :	220 240 250 240 270 human ACAAAGGTGCCAGCCTGGGGATGTTGCCCAGCTTCTTGGAAGTCATTTGGTTCCAGTTGCTACT ::::::::::::::::::::::::::::::::::
human A murine A	human (murine (human 7	human A murine A

Fig. 4

.: E	C I G C I G	C + :: C	AC -
340 ZATTTG :::::	410 ATTTTC :::: ACTTCC 410	480 AAAATGTCA ::::::: AAAATGTCA 480	550 AACCT/
AGCAC .::.	TCTT? ::::: TCTT?	AGAAP . :: GTCAP	CTGGA
310 320 330 34 AGTGAGCAGAACTGTGTTGAGATGGGAGCACAT ::::::::::::::::::::::::::::::::::::	0 370 380 390 400 AGCAGAGCAGAATTTCATTGTCCAGCAGCTGAATGAGTCATTTTCTTA ::::::::::::::::::::::::::::	470 ACACCTTATGAC ::::: ACTCCTTTCAG1	540 :AGTCTT
GTTG2	ATGA(:::: ATGA(GACAC :::: TACTC	TCAAT :::: TCAA-
320 \ACTGT :::::: \ACTGT	390 AGCTGA ::::: AGCTGA 390	0 440 450 460 CAAGGTAATAATTGGCAATGGATTGATAAG :::::::::::::::::::::::::::::::::::	530 :GTGCT ::::
GCAG2	CAGCZ:::CAGCZ	GGATI :::: GGATC	GCAAT ::: GCGGI
310 ;AGTGA :::::	380 LTTGTC : : : LTCACC 380	450 GCAAT::::: GCAAT:	520 GCAGA : ::: GAAGA 520
CTAAG ; GCACC	TTTCA ::::: TTTCA	AATTG ::::	ATTCT .: :. ITCCA
300 TTGGTCT :::. CTGGAGC 300	370 CAGAA ::::: CAGAA 370	440 ATAAT :: ATGGC 440	0 510 520 53 GTGAGCCCAATCATTCTGCAGAGCAATGT .::::::::::::::::::::::::::::::::::
AAGGT :::	CAGAG ::::	AGGTA ::::: AGGTA	SAGCC
290 GAAGAGAA .:.:::: AAGGAGAA 290	360 ACAGAAGG ::::::: ACTGAAGG	430 CCACAZ :::::	500 IAGGIG
AGTG.	AACAC: ::: AATAC'	AGAC(.:: :GGAT(CACC!
280 330 340 TCATTTCCAGTGAAGAAGGTTTGGTCTAAGAGTGAGCAGAACTGTGTTGAGATGGGAGCACATTTGGT ::::::::::::::::::::::::::::::::	350 360 410 TGTGTTCAACACAGAAGCAGAATTTCATTGTCCAGCAGCTGAATGAGTCATTTTCTTATTTTCTG ::::::::::::::::::::::::::::::::	420 430 440 450 460 470 480 GGGCTTTCAGACCACAGGTAATAATAATTGGCAATGGATTGATAAGACACCTTATGAGAAAAATGTCA ::::::::::::::::::::::::::::::::::::	490 500 510 520 530 540 550 human GATTTTGGCACCTAGGTGAGCCAATCATTCTGCAGAGCAATGTGCTTCAATAGTCTTCTGGAAACCTAC :::::::::::::::::::::::::::::::
human murine	human murine	human murine	human murine

Fig. 4

murine

human CTA

murine ---

Fig. 4K

Fig. 4L

70 ICFSEG ICFSEG 70	140 SFSYFL : .: :: SLSYFL 140	EMNKIYL .:::::
SLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLT:::::::::::::::::::::::::::::::::::	90 100 110 120 130 1 KSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSY :::::::::::::::::::::::::::::::::::	SAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKINS:::::::::::::::::::::::::::::::::::
50 HFTYGETGKRI .::: QFIMDQPSRRI 50	120 AHLVVFNTEAE :::::::: AHLVVINTEAE	190 WKPTGWGWNDV::::::::::::::::::::::::::::::::::::
40 CFIVSCVVTYI :::::::::	110 KSEQNCVEMG; ::::::::::::::::::::::::::::::::::::	180 ISAEQCASIVF :::::::::: PEERCVSIVYI 180
30 ISIALLS/ ISMLLLS1 30	100 SSEEKVWS : : : : STKENFWS 100	170 WHLGEPN! ::: WHPHEPNI
20 SWLSLRLWSVAG : .:::::: -W-TLRLWSAAV 20	90 SWKSFGSSCYFI ::::::::::	160 IDKTPYEKNVRF ::. ::::: IDDTPFSQNVRF 160
10 20 30 40 50 60 70 ht405 mmoeoopostekrgwlslrlwsvagisiallsacfivscvvtyhftygetgkrlselhsyhssltcfseg ::::::::::::::::::::::::::::::::::::	80 100 110 120 130 140 hT405 TKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL ::::::::::::::::::::::::::::::::::::	150 160 170 180 190 200 hT405 GLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIYL ::::::::::::::::::::::::::::::::::::
hT405 Dectin	hT405 'Dectin'	hT405 Dectin

Fig. 4M

60 120 178	226	274	322	370	418
GCATTTAACT AGGTCCCTGA CCTCAACA	CTG Leu	TGT Cys	CCC	TGC Cys	CCA Pro
CATTAGGE	ACC Thr 15	ACC Thr	CAG Gln	ACC Thr	TGC Cys
	TGG Trp	AGT Ser 30	GAC Asp	CIC Leu	TGC Cys
CCGCTCTGTG GACAGAAGCC TGAACATACA	TGC Cys	TTG	ATG Met 45	AGT Ser	GGA Gly
CCGC GACA TGAA	GTC Val	CTC	ATT Ile	TCC Ser 60	TGG
GGC TTT TTC	GGA Gly	TTA Leu	TTT Phe	CAT His	ATG Met
CAGCATTGGC TGGCCTCTTT CCTGACCTTC	AAG Lys 10	ATG Met	CAA Gln	TAC Tyr	AAA Lys
_	GGG G1y	TCC Ser 25	TAC Tyr	ACA Thr	GAA Glu
TCTGGGTTTG TTCTGAACTC GCAAGAAACC	CAA Gln	ATT Ile	ACT Thr 40	CAC His	TCA Ser
TGGG CTGA AAGA	TCC	GTG Val	GTG Val	CTT Leu 55	GTG Val
	CAA Gln	GCT Ala	GTG Val	GAA Glu	ATG
TGAC GTTG CAGA		GCT Ala	TGT Cys	$\mathtt{TAT}\\ \mathtt{TYr}$	ACT Thr
TCCGCTGACT TGGAAGTTGA GGAGACAGAT	GAA AGA Glu Arg 5	TCA Ser 20	AGC Ser	CTA Leu	GGG
CG TO TO THE COLUMN TH	CAG Gln	TGG Trp	GCG Ala 35	AGA Arg	GAA Glu
CGACCCCGCG CAAGTGTGTG GTCGTATTTT	GTG (Val	cTC.	ATT Ile	AGA Arg 50	AGT
CGAC	ATG Met	AGA Arg	TTC	AGT	TTC Phe

Fig. 4N

466	514	562	610	658	706
AAG Lys	GCT Ala	CAG Gln	CAA Gln	AAT Asn 160	TGT Cys
ACC Thr 95	$\texttt{GGG}\\ \texttt{G1}\underline{\texttt{y}}$	ACC Thr	CCA Pro	CAA Gln	CGG Arg 175
TCT Ser	ATG Met 110	ATC Ile	GAT Asp	AGT Ser	GAG Glu
ATT Ile	CAG Gln	TTC Phe 125	TCG Ser	TTC Phe	GAA Glu
CIC	GTT Val	AAT Asn	CTT Leu 140	CCT Pro	CCA Pro
TAC Tyr	$ ext{TGT}$	CAG Gln	GGT Gly	ACT Thr 155	CTT Leu
TGC Cys 90	AAC Asn	GAG Glu	CTG Leu	GAT Asp	AAT Asn 170
AGC Ser	CAG Gln 105	GCG Ala	TTC Phe	GAT Asp	CCC Pro
TCC	GAG Glu	GAA Glu 120	TAC Tyr	ATC Ile	GAA Glu
GGC Gly	AGT Ser	ACT	TCT Ser 135	TGG Trp	CAT His
TTT Phe	ACC Thr	AAT Asn	CTT Leu	CAA Gln 150	CCC
TCA Ser 85	AGC Ser	ATC Ile	TCA Ser	TGG Trp	CAC His 165
AAG Lys	TGG Trp 100	GTG Val	GAG Glu	AAA Lys	TGG Trp
TGG Trp	TTC Phe	GTG Val 115	AAT Asn	GGC Gly	TTC Phe
CAC His	AAC Asn	CTG Leu	CTG Leu 130	AAT Asn	AGG Arg
AAT Asn	GAG Glu	CAT His	CAG Gln	GGT Gly 145	GTC Val

754	8 0 2	8 2 8	918 978 1038 1098 1158 1218
TGG AAT GAT GTT Trp Asn Asp Val 190	AAG ATT TAC Lys Ile Tyr	TA TTCATTAATA TCTTTAAAGT TCAGACCTAC CAAGAAGCCA	CCTAGCCACT ATTCTTTACT TIGICAACTT GACACAACT CTCTGTCAGC TTGACCAGTC AGAGGGTCCA GGTGGTAAGC TCCATCCATC TCTGCCCTCA ACTGCTGTTA CTTGAAAGTA
GGC TGG AAT Gly Trp Asn 190	ATG AAG Met Lys 205	GACCTAC	CCTAGCCACT TTGTCAACTT CTCTGTCAGC AGAGGGTCCA TCCATCCATC
AAA IGG Lys Irp	TCA ATA TGT GAA ATG AAG AAT Ser Ile Cys Glu Met Lys Lys Ile 200	AAAGT TCA	CCGTTCTTTT GGTTAGAGTT AAGGAATTGC GATTGTTGTA GGGAGCATCA CTTTCTATGA AAAA
CCT Pro		AATA ICITI	CTGACAGAGG CC TCCTTCTGAT GG ATCTTCAGCT AZ CTTGATTAAT GZ GAGCAAGCCA GG GCCCTGGTTT CT
TGG Trp	CAC His	TTCATT	
GTT Val 180	AGT	CCTGTTA	GCCTGTACAT GAGCCCTTTC GGGGAGTAGG GGGGCATTTT AACCCATGAA CCAGGGTCTT
TCA ATA Ser Ile	TGT GAT Cys Asp 195	CTA TGA GTGCCTGT. Leu *	TAACTTCTTG GCCTGTACAT CAAACAGAAT GAGCCCTTTC AGAGTCACCT GGGGAGTAGG AGCATGTCTG GGGGCATTTT AAAGGTGTTA AACCCATGAA GGTTTCTGCC CCAGGGTCTT TAAGATGAAT AAACAATTTC
GTT Val	TTC Phe	CTA Leu	TAA CAA AGG AGC AAA(GGT'

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13 20 27	34	39	4 45	50	7 56	900000000000000000000000000000000000000
GG GG GT GG GTT AG	M Q S H L AACTGCTATCCACAAACACCATTAATCCTTTAGGGAGGCAGAAAAGGCCAGA ATG CAA AGC CAT CTT	G GGG	A GCT	V GTT	K AAG	AAA MTA SGG
TAAA CTTT AACTG	H CAT	G GGA	W TGG	Q CAG		E I V AGGACCCTGAGAATGGCATAGGGTAAAACTGGGACAG GCTGCAGAGGGCACGGAGGAGGAGGAGGGAGGAGAGAGAG
CTGC SCTGC SCTGC IGGAZ	S A AGO	W TGG	L	S TCT	T ACA	AACTC SGGAC SGCAI AATTI
AGCAC AGGAC FATGT	O G CAA	I ATC	N AAC	A GCT	E GAG	STAAZ SAGAC AATGC CTATZ AATCZ
CCTTESACAE	M A ATC	FTTT	S AGT	$_{ m TTA}$	K AAG	TAGGC AGAAC TAAAA ACATC STAAA
SAACI ACATO SGCTI	CCAG	A GCC	D GAC	M ATG	E GAG	GGCA' AAGG' CCAA' CTCA' ATGG(
TGAGG ACAGZ ACAGG	AAGG	W TGG	Q CAG	R AGG	H CAT	GAAT(GAACG) GAAC(TATG(GAGA)
CTCC: CCCTZ CCCTZ CTGGZ	AGAA	L	G GGC	E GAA	R CGA	CTGA GAGG CAAA AAAA TGAT
CACC	AGGC	L	P CCT	W TGG	G GGA	GACC GAGG AAGA CATA ACAC GAGG
CAAT(TGGTT GGTT/ TAAC/	AGGG,	$_{ m TTA}$	E GAG	E GAA	K AAA	TAA GACA TAAG AATA CTAC
TCCA(ACAC' GGAA(CACT'	CTTT	F TTT	S AGT	R AGG	E GAG	V GTG GAGGC TTCA1 AATA/ ACCA(
CCAT' IGTC' ITGG(AATC	V GTC	N AAC	N AAT	E GAA	I ATA TGCA(TACA! GGCC! AGAT!
GAAA(ATAT' ATGA' ATGG;	CATT	S TCT	W TGG	S TCT	GGA	E GAG TAGCT ACAAT GAGTG TGTGA
TCCG TCAG GCCT	ACAC	GGG	T ACT	I ATT	G GGA	G E G GGT GAG GGG G STGGGAGAACGATA SGAGAACTCTCAC AGATGATATATTGA AATTAAAAGCACTG
CGCG'GTAA'CCTT(CTTAA'TAAA'	ACAA	L CTA	CCC	I ATT	P	E GAG GAGA AAAC GATA AAAA
CCCA(GTTT) IGCT(ATCC	T ACA	S TCC	D GAC	C TGT	GGT GGTG GGAG AGAT AATT
GTCGACCCACGCGTCCGGAAACCATTCCACAATCACCCTCCTGAGGAACTCTTAGCACTGCATAAAGT GTTCTGAGTTTGTAATCAGATATTGTCACACTGGTTCCTTCAAACAGGACATGACAAGGAGCTGGCTTTGG GCTAGGCTGCTCCTTGCCTATGATTGGGGAAGGTTAAACCCCTACAGGGCTTATGTATG	TGCT	F I T L G S V F L L L W A F I W G G TTC ATT ACA CTA GGG TCT GTC TTT TTA CTT CTC TGG GCC TTT ATC TGG GGA GGG	V GTT	C D D I I S N R E W E R M L A S Q TGT GAT GAC ATT ATT AGT GAA TGG GAA AGG ATG TTA GCT TCT CAG	K . AAG	K M G E G AAG ATG GGT GAG GGG G AGATACTGTGGGAGAACGATA ACAGTTTGGAGAAACTCTCAC CCACAGAGATGATATTTGA AAATGCAAATTAAAAGCACTG
GTT GCT GCT	AAC	F TTC	H CAI	C TGT	L TTA	K AAG ACA CCA AAA

Fig. 5A

The first state of the state of

GTGAAAACCCTGTCTCTACTAAAACATACAAAATTAGCTGGGGGTGGTGGCATGCGCCTGTAATTCCAGCT	1043
ACTICACION CALCONO CONTROL DE LA CONTROL DE	1113
CCTTCTACTACTACTACTCCTCCTCTCACAGAGCGAGACTCTTAAAAAAAA	1183
	1202

Fig. 5B

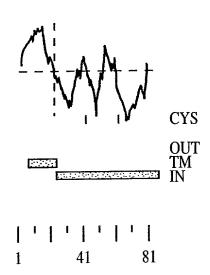


FIG. 5C